

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 12.81 Seconds
(without alignments)
35.679 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	77	2 A01259	complement C3 - pi
2	30	100.0	111	2 I48204	colipase - nutria
3	30	100.0	351	1 MFN2B3	matrix protein - p
4	30	100.0	401	2 T46306	hypothetical prote
5	30	100.0	530	1 G64918	phosphotransferase
6	30	100.0	530	2 F85768	PTS system, maltos
7	30	100.0	584	2 S06696	hypothetical prote
8	30	100.0	1009	2 D75399	probable penicilli
9	28	93.3	230	2 H83001	probable permease
10	28	93.3	285	2 T12342	major intrinsic pr
11	28	93.3	494	2 S16068	testosterone 15alp
12	28	93.3	494	2 B33531	cytochrome p450 2A
13	28	93.3	494	2 B47494	cytochrome p450 2A
14	28	93.3	494	2 A32030	coumarin 7-monoxy
15	28	93.3	494	2 A33531	testosterone 15alp
16	28	93.3	527	2 F83368	probable aldehyde
17	27	90.0	132	2 T29072	hypothetical prote
18	27	90.0	175	2 G72683	hypothetical prote
19	27	90.0	179	2 S65534	light-harvesting c
20	27	90.0	190	2 T29068	hypothetical prote
21	27	90.0	202	2 C84305	hypothetical prote
22	27	90.0	213	2 S75247	hypothetical prote
23	27	90.0	256	2 F96510	light-harvesting c
24	27	90.0	256	2 T52328	chlorophyll a/b-bi
25	27	90.0	280	2 T04049	chlorophyll a/b-bi
26	27	90.0	286	2 S16294	chlorophyll a/b-bi
27	27	90.0	302	2 S31865	chlorophyll a/b-bi
28	27	90.0	376	2 E70680	probable prob - My
29	27	90.0	379	2 C81809	hypothetical prote

ALIGNMENTS

RESULT 1

A01259

N:Complement C3 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: A01259

R:Corbin, N.C.; Hugli, T.E.

J. Immunol. 117, 990-995, 1976

A:Title: The primary structure of porcine C3a anaphylatoxin.

A:Reference number: A01259; MUID:76263261

A:Accession: A01259

A:Molecule type: protein

A:Residues: 1-77 <COR>

A:Note: three disulfide bonds are present

C:Comment: Complement C3 contains two chains, formed by removal of four residues and
alternative complement pathways, releases the C3a anaphylatoxin from the amino end o
native-complement-pathway C3/C5 convertase.

C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.

C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign

e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by

C:Comment: The major site of synthesis of this plasma protein is the liver.

C:Superfamily: alpha-2-macroglobulin

C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprote

F:1-77/Product: complement C3a anaphylatoxin #status experimental <C3A>

Query Match 100.0%; Score 30; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 72 PLGLAR 77

RESULT 2

I48204

colipase - nutria

C:Species: Myocastor coypus (nutria, coypu)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999

C:Accession: I48204

R:Thirstrup, K.; Carriere, F.; Hjorth, S.A.; Rasmussen, P.B.; Nielsen, P.F.; Ladefog

Eur. J. Biochem. 227, 186-193, 1995

A:Title: Cloning and expression in insect cells of two pancreatic lipases and a proco

A:Reference number: I48204; MUID:95154288

A:Accession: I48204

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-111 <RES>

A:Cross-references: EMBL:X82998; MID:g599866; PIDN:CAA58119.1; PTD:g599867

C:Superfamily: colipase

probable cation-tr
heat shock protein
leukemia virus cel
al-mating type pro
probable 3-demethy
hypothetical prote
ChrA protein - Erw
NADH dehydrogenase
probable periplasm
hypothetical prote
fructose-6-P phosph
pyrophosphate--fru
hypothetical prote
fructose-6-P phosph
oxalyl-CoA decarbo
penicillin-binding

```

Query Match          100.0%; Score 30; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 50 PLGLAR 55

RESULT 3
MFNBZ3
matrix protein - parainfluenza virus type 3
C:Species: parainfluenza virus type 3
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C:Accession: D27502
R:Sakai, Y.; Suzu, S.; Shioda, T.; Shibuta, H.
Nucleic Acids Res. 15, 2927-2944, 1987
A:Title: Nucleotide sequence of the bovine parainfluenza 3 virus genome: its 3' end and
A:Reference number: A93658; MUID:87174818
A:Accession: D27502
A:Molecule type: genomic RNA
A:Residues: 1-351 <SAK>
A:Cross-references: EMBL:X00114; NID:g60891; PIDN:CAA68296.1; PID:g60895
C:Genetics:
A:Gene: M
C:Superfamily: parainfluenza virus matrix protein
C:Keywords: matrix protein

Query Match          100.0%; Score 30; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 93 PLGLAR 98

RESULT 4
T46306
hypothetical protein DKF2p434D2411.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C:Accession: T46306
R:Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A:Reference number: 223035
A:Accession: T46306
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-401 <AAA>
A:Cross-references: EMBL:AL137599
A:Experimental source: adult testis; clone DKF2p434D2411
C:Genetics:
A:Note: DKF2p434D2411.1

Query Match          100.0%; Score 30; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 126 PLGLAR 131

RESULT 5
G64918
phosphotransferase system enzyme II (EC 2.7.1.69) factor II, maltose- and glucose-specific
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: G64918; B42477; PV0011
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64918
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-530 <BLAT>
A:Cross-references: GB:AE000258; GB:U00096; NID:g2367121; PIDN:AACT4693.1; PID:g17879
A:Experimental source: strain K-12, substrain MG1655
R:Reidl, J.; Boos, W.
J. Bacteriol. 173, 4862-4876, 1991
A:Title: The malX maly operon of Escherichia coli encodes a novel enzyme II of the ph
alose system.
A:Reference number: A42477; MUID:91310596
A:Accession: B42477
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-143, 'Y', 145-295, 'N', 297-431, 'R', 433-530 <REI>
A:Cross-references: GB:M60722; NID:g146690; PIDN:AAA24098.1; PID:g146692
R:Reidl, J.; Roemisch, K.; Ehrmann, M.; Boos, W.
J. Bacteriol. 171, 4888-4899, 1989
A:Title: MalX, a novel protein involved in regulation of the maltose system of Escher
A:Reference number: JV0031; MUID:89359124
A:Accession: PV0011
A:Molecule type: DNA
A:Residues: 1-119, 'AFCOPRMPRLKRRTKNAKAFHDKMRKLTFRASNETDVLITAFYSLHGDPREF' <RE2>
A:Cross-references: GB:M28539; NID:g146707; PIDN:AAA24103.1; PID:g146708
C:Genetics:
A:Gene: malX
A:Map position: 36 min
C:Function:
A:Description: mediates transport of glucose and maltose across the cytoplasmic membr
r concentration
C:Superfamily: phosphotransferase system glucose-specific enzyme II, factor II; phosph
C:Keywords: phosphoprotein; phosphotransferase; sugar transport system; transmembrane
F:7-528/Domain: phosphotransferase system glucose-specific enzyme II, factor II homol
F:22-38/Domain: transmembrane #status predicted <TM01>
F:73-89/Domain: transmembrane #status predicted <TM02>
F:99-115/Domain: transmembrane #status predicted <TM03>
F:146-162/Domain: transmembrane #status predicted <TM04>
F:185-201/Domain: transmembrane #status predicted <TM05>
F:321-337/Domain: transmembrane #status predicted <TM06>
F:354-370/Domain: transmembrane #status predicted <TM07>
F:399-415/Domain: transmembrane #status predicted <TM08>
F:493-510/Domain: transmembrane #status predicted <TM09>
F:471/Active site: Cys (phosphocysteine intermediate) #status predicted

Query Match          100.0%; Score 30; DB 1; Length 530;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
    |||||
Db 86 PLGLAR 91

RESULT 6
F85768
PTS system, maltose and glucose-specific II ABC [imported] - Escherichia coli (strain
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85768
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A95480; MUID:21074935; PMID:11206551
A:Accession: F85768
A>Status: preliminary

```

Qy 1 plglar 6
|||||

RESULT 11
SL6068
testosterone 15alpha-monooxygenase (EC 1.14.14.-) cytochrome P450 2A3 isoform 2 - mouse
N:Alternate names: cytochrome P450(15-alpha); testosterone 15alpha-hydroxylase
C:Species: Mus musculus (house mouse)
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 04-Mar-2000
C:Accession: SL6068
R:Squires, E. J.; Negishi, M.
J. Biol. Chem. 263, 4166-4171, 1988

A:Title: Reciprocal regulation of sex-dependent expression of testosterone 15-alpha-hydroxysteroid oxidoreductase (EC 1.1.1.61)
A:Reference number: S16067; MUID:88153731
A:Accession: S16068
A:Molecule type: mRNA
A:Residues: 1-494 <SQ>
A:Cross-references: EMBL:M19319
C:Genetics:
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metalloprotein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 12
B33531
cytochrome P450 2A3.2 - mouse
N:Contains: oxidoreductase (EC 1.1.1.61)
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 04-Mar-2000
C:Accession: B33531; B30499
R:Jindberg, R.; Burkhardt, B.; Ichikawa, T.; Negishi, M.
J. Biol. Chem. 264, 6465-6471, 1989
A:Title: The structure and characterization of type I P-450-15-alpha gene as major steroid hydroxylase
A:Reference number: A33531; MUID:89197954
A:Accession: B33531
A:Molecule type: DNA
A:Residues: 1-494 <LIN>
A:Cross-references: GB:M25211; GB:J04631; NID:g193826; PIDN:AAA37798.1; PID:g387191
A:Accession: B30499
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-494 <li2>
A:Cross-references: GB:M25211; GB:J04631; NID:g193826; PIDN:AAA37798.1; PID:g387191
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 13
B47494
cytochrome P450 2A11 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 04-Mar-2000
C:Accession: B47494; JC2553
R:Peng, H.M.; Ding, X.; Coon, M.J.
J. Biol. Chem. 268, 17253-17260, 1993
A:Title: Isolation and heterologous expression of cloned cDNAs for two rabbit nasal mucin glycoproteinase genes
A:Reference number: A47494; MUID:93352510
A:Accession: B47494
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-494 <PEN>
A:Cross-references: GB:L10237; NID:g165434; PIDN:AAA31372.1; PID:g165435

R:Ding, X.; Peng, H.M.; Coon, M.J.
Biochem. Biophys. Res. Commun. 203, 373-378, 1994
A:Title: Structure-function analysis of CYP2A10 and CYP2A11, P450 cytochromes that di
A:Reference number: JC2552; MUID:94354829
A:Contents: annotation
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; transmembrane protein
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 14
A32030
cumarin 7-monooxygenase (EC 1.14.14.-) cytochrome P450 2A3 - rat
N:Alternate names: coumarin 7-hydroxylase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 08-Feb-1996 #text_change 28-Jul-2000
C:Accession: S15056; S12708; A32030
R:Ueno, T.; Gonzalez, F.
submitted to the EMBL Data Library, March 1990
A:Description: Complete sequence of the rat CYP2A3 gene specifically transcribed in l
A:Reference number: S15056
A:Accession: S15056
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <UEN>
A:Cross-references: EMBL:M33190; NID:g203750; PIDN:AAA41022.1; PID:g203751
R:Ueno, T.; Gonzalez, F.J.
Nucleic Acids Res. 18, 4623-4624, 1990
A:Title: Complete sequence of the rat CYP2A3 gene specifically transcribed in lung.
A:Reference number: S12708; MUID:90356430
A:Accession: S12708
A:Molecule type: DNA
A:Residues: 1-108, 'G', 110-334, 'N', 336-494 <UE2>
A:Cross-references: EMBL:M33190
A:Note: the authors translated the codon AAG for residue 326 as Leu, TTT for residue
R:Kimura, S.; Kozak, C.A.; Gonzalez, F.J.
Biochemistry 28, 3798-3803, 1989
A:Title: Identification of a novel P450 expressed in rat lung: cDNA cloning and sequ
A:Reference number: A32030; MUID:89323084
A:Accession: A32030
A:Molecule type: mRNA
A:Residues: 8-108, 'G', 110-334, 'N', 336-494 <KIM>
A:Cross-references: GB:J02852; NID:g703260; PIDN:AAA88511.1; PID:g703261
C:Genetics:
A:Gene: CYP2A3
A:Introns: 60/3; 115/1; 165/1; 218/3; 277/3; 325/1; 387/3; 435/1
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; meta
F:298-461/Domain: cytochrome P450 homology <P45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
|:||||
Db 367 PMGLAR 372

RESULT 15
A33531

testosterone 15alpha-monooxygenase (EC 1.14.14.-) cytochrome P450 2a4 - mouse
N:Alternate names: cytochrome P450(15-alpha) I
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1992 #sequence.Revision 31-Mar-1992 #text_change 03-Nov-2000
C:Accession: A33531; A30499; S16067; I55275; I70052
R:Lindberg, R.; Burkhardt, B.; Ichikawa, T.; Negishi, M.
J. Biol. Chem. 264, 6465-6471, 1989
A:Title: The structure and characterization of type I P-450-15-alpha gene as major steroid
A:Reference number: A33531; MUID:89197954
A:Accession: A33531
A:Molecule type: DNA
A:Residues: 1-494 <LIN1>
A:Cross-references: GB:M26208; GB:J04631; NID:gl93816; PIDN:AAA37797.1; PID:g387190
A:Accession: A30499
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-494 <LIN2>
A:Cross-references: GB:M26208; GB:J04631; NID:gl93816; PIDN:AAA37797.1; PID:g387190
R:Squires, E.J.; Negishi, M.
J. Biol. Chem. 263, 4166-4171, 1988
A:Title: Reciprocal regulation of sex-dependent expression of testosterone 15-alpha-hydroxylase
A:Reference number: S16067; MUID:88153731
A:Accession: S16067
A:Molecule type: mRNA
A:Residues: 1-295, 'Q', 297-305, 'G', 307-494 <SQU>
A:Cross-references: EMBL:J03549; NID:g201970; PIDN:AAA40426.1; PID:g201971; GB:M19319; N
C:Genetics:
A:Gene: Cyp2a4
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F:298-461/Domain: cytochrome P450 homology <p45>
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 93.3%; Score 28; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Oy 1 plg1ar 6
|:|:|:|
Db 367 FMGLAR 372

Search completed: February 28, 2002, 16:47:23
Job time: 78 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:25 ; Search time 10.14 seconds
(without alignments)
21.695 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 piglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	77	1	CO3A_PIG
2	30	100.0	111	1	COL_MYOCO
3	30	100.0	351	1	VMAT_PT3B
4	30	100.0	530	1	PTOA_ECOLI
5	30	100.0	584	1	65KD_ZYMMO
6	30	100.0	867	1	SSPO_BOVIN
7	28	93.3	142	1	DKSA_CAUCR
8	28	93.3	421	1	SNAA_STRPR
9	28	93.3	494	1	CPA3_RAT
10	28	93.3	494	1	CPA4_MOUSE
11	28	93.3	494	1	CPA5_MOUSE
12	28	93.3	494	1	CPAB_RABIT
13	27	90.0	376	1	PROB_MYCTU
14	27	90.0	631	1	DXS_STRCL
15	27	90.0	679	1	HSR2_AJECA
16	27	90.0	843	1	BLVR_BOVIN
17	26	86.7	233	1	TNFA_TRIVU
18	26	86.7	305	1	CBRA_ERWCH
19	26	86.7	394	1	NUCM_ARATH
20	26	86.7	439	1	YT55_STRFR
21	26	86.7	526	1	MEMA_METFR
22	26	86.7	554	1	Y514_SYNY3
23	26	86.7	568	1	OXC_OXAFO
24	26	86.7	853	1	PBPA_HAFIN
25	26	86.7	1050	1	ULK1_HUMAN
26	25	83.3	114	1	CH60_MYCUL
27	25	83.3	116	1	CB2D_LYCES
28	25	83.3	120	1	CH60_MYCAG
29	25	83.3	120	1	CH60_MYCAS
30	25	83.3	120	1	CH60_MYCCI
31	25	83.3	120	1	CH60_MYCFA
32	25	83.3	120	1	CH60_MYCGN
33	25	83.3	120	1	CH60_MYCGO

34	25	83.3	120	1	CH60_MYCGS
35	25	83.3	120	1	CH60_MYCIT
36	25	83.3	120	1	CH60_MYCKA
37	25	83.3	120	1	CH60_MYCNO
38	25	83.3	120	1	CH60_MYCPH
39	25	83.3	120	1	CH60_MYCPV
40	25	83.3	120	1	CH60_MYCRH
41	25	83.3	120	1	CH60_MYCVA
42	25	83.3	127	1	CB21_EUGGR
43	25	83.3	143	1	YBIF_SALTY
44	25	83.3	150	1	CB22_PINSY
45	25	83.3	151	1	CH60_MYCAV

ALIGNMENTS

RESULT 1
CO3A_PIG
ID CO3A_PIG STANDARD; PRT; 77 AA.
AC P01025;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE COMPLEMENT C3A ANAPHYLATOXIN.
DE C3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=76263261; PubMed=956663;
RA Corbin N.C., Hugli T.E.;
RT "The primary structure of porcine C3a anaphylatoxin.";
RL J. Immunol. 117:990-995(1976).
CC -1- FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
BASOPHILIC LEUKOCYTES.
CC -1- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
DR PIR; A01259; C3PGAT.
DR HSSP; P01031; LKJS.
DR InterPro: IPR001599; Alpha_2_macroglubln.
DR InterPro: IPR000020; Anaphylatoxin.
DR InterPro: IPR001840; Anaphylatoxn.
DR Pfam; PF01821; ANATO; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
KW Complement pathway; Complement alternate pathway; Plasma;
FT Inflammatory response.
FT DOMAIN 22 57 ANAPHYLATOXIN-LIKE.
FT DISULFID 22 49 BY SIMILARITY.
FT DISULFID 23 56 BY SIMILARITY.
FT DISULFID 36 57 BY SIMILARITY.
SQ SEQUENCE 77 AA; 9085 MW; 7ECB22E619533429 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 piglar 6
Db 72 PLGLAR 77

RESULT 2
COL_MYOCO

```
ID COL_MYOCO STANDARD; PRT; 111 AA.
AC P42889;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE COLIPASE PRECURSOR.
GN CLPS.

OS Myocastor copys (Coypu) (Nutra).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-41.
RC MEDLINE=95154288; PubMed=7851384;
RX Thirstup K., Carrier F., Hjorth S.A., Rasmussen P.B., Nielsen P.F.,
RA Ladefoged C., Thim L., Boel E.;
RT "Cloning and expression in insect cells of two pancreatic lipases and
a procollipase from Myocastor copys.";
RL Eur. J. Biochem. 227:186-193(1995).
CC -!- FUNCTION: COLIPASE IS A COFACTOR OF PANCREATIC LIPASE. IT ALLOWS
THE LIPASE TO ANCHOR ITSELF TO THE LIPID-WATER INTERFACE. WITHOUT
COLIPASE THE ENZYME IS WASHED OFF BY BILE SALTS, WHICH HAVE AN
INHIBITORY EFFECT ON THE LIPASE.
CC -!- FUNCTION: ENTEROSTATIN HAS A BIOLOGICAL ACTIVITY AS A SATIETY
SIGNAL (BY SIMILARITY).
CC -!- SUBUNIT: FORM A 1:1 STOICHIOMETRIC COMPLEX WITH PANCREATIC LIPASE.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X82998; CAA58119.1; -.
CC HSP; P02703; IPCO.
CC InterPro: IPR001981; Collipase.
CC Pfam: PF01114; Collipase; 1.
CC PRINTS: PR00128; COLIPASE.
CC SMART: SM00023; COLIPASE; 1.
CC PROSITE: PS00121; COLIPASE; 1.
KW Lipid degradation; Digestion; Pancreas; Signal.
FT SIGNAL 1 17
FT PROPEP 18 22 ENTEROSTATIN, ACTIVATION PEPTIDE
(POTENTIAL).
FT CHAIN 23 111
FT DISULFID 34 45 BY SIMILARITY.
FT DISULFID 40 56 BY SIMILARITY.
FT DISULFID 44 78 BY SIMILARITY.
FT DISULFID 66 86 BY SIMILARITY.
FT DISULFID 80 104 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11899 MW; 7FF37DE7C169616B CRC64;
```

Query Match 100.0%; Score 30; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
|||||
DB 50 PLGLAR 55

RESULT 3

```
ID VMAAT_PT3B STANDARD; PRT; 351 AA.
AC P06166;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
```

```
DE MATRIX PROTEIN.
GN M.
OS Bovine parainfluenza 3 virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.
OX NCBI_TaxID=11215;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=910N;
RX MEDLINE=87174818; PubMed=3031614;
RA Sakai Y., Suzu S., Shioda T., Shibuta H.;
RT "Nucleotide sequence of the bovine parainfluenza 3 virus genome: its
3' end and the genes of NP, P, C and M proteins.";
RL Nucleic Acids Res. 15:2927-2944(1987).
CC -!- FUNCTION: THE M PROTEIN HAS A CRUCIAL ROLE IN VIRUS ASSEMBLY
AND INTERACTS WITH THE RNP COMPLEX AS WELL AS WITH THE VIRAL
MEMBRANE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00114; CAA68296.1; -.
CC EMBL; D84095; BAA12216.1; -.
CC PIR; D27502; MFNZB3
CC InterPro: IPR000982; Matrix.
CC Pfam: PF00861; Matrix; 1.
CC ProDom: PD000741; Matrix; 1.
KW Matrix protein; Envelope protein.
SQ SEQUENCE 351 AA; 39310 MW; C7749FC19EA79535 CRC64;
```

Query Match 100.0%; Score 30; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
|||||
DB 93 PLGLAR 98

```
RESULT 4
ID PTOA_ECOLI STANDARD; PRT; 530 AA.
AC P19642; P77621;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PTS SYSTEM. MALTOSE AND GLUCOSE-SPECIFIC IIABC COMPONENT (MALTOSE AND
GLUCOSE-PERMEASE IIABC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, ABC
COMPONENT) (EC 2.7.1.69).
GN MALX OR B1621.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91310596; PubMed=1856179;
RA Reidl J., Boos W.;
RT "The malX maly operon of Escherichia coli encodes a novel enzyme II
of the phosphotransferase system recognizing glucose and maltose and
an enzyme abolishing the endogenous induction of the maltose
system.";
RL J. Bacteriol. 173:4862-4876(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
```

RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RC MEDLINE=97251357; PubMed=9097039;
 RX Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
 RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
 RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,
 RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,
 RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
 RA Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [4]
 RN PRELIMINARY SEQUENCE OF 1-177 FROM N.A.
 RX MEDLINE=89359124; PubMed=2670898;
 RA Reidel J., Romisch K., Ehrmann M., Boos W.;
 RT "MalI, a novel protein involved in regulation of the maltose system
 RT of *Escherichia coli*, is highly homologous to the repressor proteins
 RT GalR, CytR, and LacI.";
 RL J. Bacteriol. 171:4888-4899(1989).
 CC -1- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
 CC SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
 CC -TRANSPORT SYSTEM. THE IIIC DOMAINS CONTAIN THE SUGAR BINDING SITE
 CC AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
 CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
 CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
 CC THE SUGAR.
 CC -1- FUNCTION: MALX ENCODES A PHOSPHOTRANSFERASE SYSTEM ENZYME II THAT
 CC CAN RECOGNIZE GLUCOSE AND MALTOSE AS SUBSTRATES EVEN THOUGH THESE
 CC SUGARS MAY NOT REPRESENT THE NATURAL SUBSTRATES OF THE SYSTEM.
 CC -1- CATALYTIC ACTIVITY: PROTEIN N-PHOSPHOISTIDINE + SUGAR =
 CC PROTEIN HISTIDINE + SUGAR PHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
 CC -1- SIMILARITY: CONTAINS A PTS EIIA DOMAIN.
 CC -1- SIMILARITY: CONTAINS A PTS EIIIB DOMAIN.
 CC -1- SIMILARITY: CONTAINS A PTS EIIC DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M60722; AAA24098.1; -;
 CC EMBL; AE000258; AAC74693.1; -;
 CC EMBL; D90805; BAA15372.1; -;
 CC EMBL; D90806; BAA15379.1; -;
 CC EMBL; D90808; BAA15409.1; -;
 CC EMBL; M28539; BAA24103.2; ALT_SEQ.
 CC PIR; PV0011; PV0011.
 CC PIR; B42477; B42477.
 CC HSP; P05053; IIBA.
 CC EcoGene; EG10563; malX.
 CC InterPro; IPR001996; PTS_EIIB.
 CC InterPro; IPR003352; PTS_EIIC.
 CC Pfam; PF00367; PTS_EIIB; 1.
 CC Pfam; PF02378; PTS_EIIC; 1.
 CC ProDom; PD001476; PTS_EIIB; 1.
 CC ProSITE; PS01035; PTS_EIIB_CYS; 1.
 CC Phosphotransferase system; Sugar transport; Transferase;
 KW Transmembrane; Inner membrane; Phosphorylation; Complete proteome.
 FT DOMAIN 1 ? EIIA DOMAIN

FT DOMAIN ? ?
 FT DOMAIN 452 486 EIIIC DOMAIN.
 FT MOD_RES 240 240 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 356 356 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 471 471 PHOSPHORYLATION (BY SIMILARITY).
 FT TRANSMEM 22 42 POTENTIAL.
 FT TRANSMEM 47 67 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 96 116 POTENTIAL.
 FT TRANSMEM 138 158 POTENTIAL.
 FT TRANSMEM 189 209 POTENTIAL.
 FT TRANSMEM 227 247 POTENTIAL.
 FT TRANSMEM 289 309 POTENTIAL.
 FT TRANSMEM 321 341 POTENTIAL.
 FT TRANSMEM 343 363 POTENTIAL.
 FT TRANSMEM 369 389 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT CONFLICT 144 144 I -> Y (IN REF. 1).
 FT CONFLICT 296 296 P -> N (IN REF. 1).
 FT CONFLICT 432 432 E -> R (IN REF. 1).
 SQ SEQUENCE 530 AA; 56627 MW; 042E9817955975BF CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 530;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 plglar 6
 Db 86 PLGLAR 91
 RESULT 5
 65KD_ZYMMO STANDARD; PRT; 584 AA.
 ID 65KD_ZYMMO
 AC P15255;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE 65 KDA PROTEIN (ORF 1).
 OS Zymomonas mobilis.
 OG Plasmid pZM2.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae.
 OC Zymomonas.
 OX NCBI_TaxID=542;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10988 / ZM1;
 RA Misawa N., Nakamura K.;
 RT "The nucleotide sequence of the 2.7 kilobase pair plasmid of *Zymomonas*
 RT mobilis ATCC 10988.";
 RL J. Biotechnol. 12:63-70(1989).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X14438; CAA32611.1; -;
 CC PIR; S06696; S06696.
 CC InterPro; IPR001668; Mob_Pre.
 CC InterPro; IPR002936; Toprim.
 CC Pfam; PF01076; Mob_Pre; 1.
 CC Pfam; PF01751; Toprim; 1.
 CC SMART; SM00493; TOPRIM; 1.
 KW Plasmid.
 SQ SEQUENCE 584 AA; 65793 MW; 0402D2FB569B65A6 CRC64;
 Query Match 100.0%; Score 30; DB 1; Length 584;

Best Local Similarity 100.0%; Pred. NO. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p1glar 6
DB 170 PLGLAR 175

RESULT 6

SSPO_BOVIN STANDARD; PRT; 867 AA.
AC P98167; DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE SCO-SPONDIN (FRAGMENT).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ependymocyte;
RX MEDLINE=96338614; PubMed=8743952;
RA Gobron S., Monnerie H., Meinzel R., Creveaux I., Lehmann W.,
RA Lamalle D., Dastuque B., Meinzel A.;
RT "SCO-spondin: a new member of the thrombospondin family secreted by
RT the subcommissural organ is a candidate in the modulation of neuronal
RT aggregation.";
RL J. Cell Sci. 109:1053-1061(1996).
CC -!- FUNCTION: INVOLVED IN THE MODULATION OF NEURONAL AGGREGATION.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: SUBCOMMISSURAL ORGAN.
CC -!- DEVELOPMENTAL STAGE: EMBRYO.
CC -!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.
CC -!- SIMILARITY: CONTAINS AT LEAST 2 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS AT LEAST 1 F5/8 TYPE C DOMAIN.
CC -!- SIMILARITY: CONTAINS AT LEAST 3 LDL-RECEPTOR CLASS A DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; X93922; CAA63815.1; -.
CC HSSP; P01130; IAJJ.
CC InterPro; IPR000421; FA58_C.
CC InterPro; IPR002172; LDL_recept_A.
CC InterPro; IPR002919; TIL.
CC InterPro; IPR000884; TSP1.
CC InterPro; IPR001007; VWFC.
CC Pfam; PF00754; F5_F8_type_C; 1.
CC Pfam; PF00057; ldl_recept_a; 3.
CC Pfam; PF01826; TIL; 1.
CC Pfam; PF00090; tsp_1; 4.
CC Pfam; PF00093; vwc; 1.
CC SMART; SM00231; FA58C; 1.
CC SMART; SM00192; LDLa; 3.
CC SMART; SM00209; TSP1; 4.
CC SMART; SM00214; VWC; 1.
CC SMART; SM00011; VWC_def; 1.
CC PROSITE; PS01285; FA58C_1; 1.
CC PROSITE; PS01286; FA58C_2; 1.
CC PROSITE; PS01209; LDLRA_1; 3.
CC PROSITE; PS00668; LDLRA_2; 3.
CC PROSITE; PS00092; TSP1; 4.
CC GlycoProtex; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
KW Glycoprotein; Cell adhesion; Calcium-binding; Repeat; EGF-like domain.
FT NON_TER

FT DOMAIN 26 81 TSP TYPE-1 1.
FT DOMAIN 103 142 EGF-LIKE 1.
FT DOMAIN 143 180 EGF-LIKE 2.
FT DOMAIN 185 243 TSP TYPE-1 2.
FT DOMAIN 344 502 F5/8 TYPE C.
FT DOMAIN 506 544 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 663 701 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 723 761 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 762 813 TSP TYPE-1 3.
FT DOMAIN 814 867 TSP TYPE-1 4.
FT DISULFID 107 122 BY SIMILARITY.
FT DISULFID 116 127 BY SIMILARITY.
FT DISULFID 129 141 BY SIMILARITY.
FT DISULFID 147 166 BY SIMILARITY.
FT DISULFID 149 169 BY SIMILARITY.
FT DISULFID 171 179 BY SIMILARITY.
FT DISULFID 344 502 BY SIMILARITY.
FT DISULFID 508 520 BY SIMILARITY.
FT DISULFID 515 533 BY SIMILARITY.
FT DISULFID 527 542 BY SIMILARITY.
FT DISULFID 665 677 BY SIMILARITY.
FT DISULFID 672 690 BY SIMILARITY.
FT DISULFID 684 699 BY SIMILARITY.
FT DISULFID 725 737 BY SIMILARITY.
FT DISULFID 732 750 BY SIMILARITY.
FT DISULFID 744 759 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 409 409 N-LINKED (GLCNAC. .) (POTENTIAL).
FT NON_TER 867 867
SQ SEQUENCE 867 AA: 91817 MW: 9538F2108E787B49 CRC64;

Query Match 100.0%; Score 30; DB 1; Length 867;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 p1glar 6
DB 347 PLGLAR 352

RESULT 7

DKSA_CAUCR STANDARD; PRT; 142 AA.
ID DKSA_CAUCR AC 032347;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE DNK SUPPRESSOR PROTEIN HOMOLOG.
GN DKSA OR CC2580.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB15N / NA1000;
RX MEDLINE=98215187; PubMed=9555902;
RA Mohr C.D., Mackichan J.K., Shapiro L.;
RT "A membrane-associated protein, Flx, is required for an early step in
RT Caulobacter flagellar assembly.";
RL J. Bacteriol. 180:2175-2185(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.K.R., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

```

RA Salzberg S.L., Shapiro L., Venter J.C., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RP SEQUENCE OF 1-76 FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RA Ely B.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 DKSA/TRAR-TYPE ZINC FINGER.
CC -!- SIMILARITY: IN THE N-TERMINAL HALF, TO THE N-TERMINAL OF
CC B. SUBTILIS YTEA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF034413; AAC38353.1; -
CC EMBL; AE005926; AAK24550.1; -
CC EMBL; M91448; AAB83954.1; -
CC TIGR; CC2580; -
CC InterPro; IPR000962; Znf_dskA_trar.
CC Pfam; PF01258; zf_dskA_trar; 1.
CC PRINTS; PR00618; DKSZNFINGER.
CC PROSITE; PS01102; DKSA_TRAR_ZN_FINGER; FALSE_NEG.
CC Zinc-finger; Complete proteome
CC ZN_FING 104 128 TRAR/DKSA-TYPE.
CC CONFLICT 137 137 R -> P (IN REF. 1).
CC SEQUENCE 142 AA; 16774 MW; 8824F2DD9827B89C CRC64;
CC -----
Query Match 93.38; Score 28; DB 1; Length 142;
Best Local Similarity 83.38; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 plglar 6
Db 110 PIGLAR 115
RESULT 8
ID SNAI_STRPR STANDARD; PRT; 421 AA.
AC P54991;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE PRISTINAMYCIN IIA SYNTHASE SUBUNIT A (PIIA SYNTHASE SUBUNIT A).
GN SNAI.
OS Streptomyces pristinaespiralis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=38300;
RN SEQUENCE FROM N.A.
RC STRAIN=SP92;
RX MEDLINE=95394837; PubMed=7665509;
RA Blanc V., Lequeux D., Didier P., Gil P., Lacroix P., Crouzet J.;
RT "Cloning and analysis of structural genes from Streptomyces
RT pristinaespiralis encoding enzymes involved in the conversion of
RT pristinamycin IIB to pristinamycin IIA (PIIA); PIIA synthase and
RT NADH:riboflavin 5'-phosphate oxidoreductase.";
RL J. Bacteriol. 177:5206-5214(1995).
RN [2]
RP SEQUENCE OF 1-18 AND 364-383.
RX MEDLINE=95394836; PubMed=7665508;
RA Thibaut D., Ratet N., Bisch D., Faucher D., Debussche L., Blanche F.;
RT "Purification of the two-enzyme system catalyzing the oxidation of
RT the D-proline residue of pristinamycin IIB during the last step of
RT pristinamycin IIA biosynthesis.";

```

```

RL J. Bacteriol. 177:5199-5205(1995).
CC -!- FUNCTION: CATALYZES THE OXIDATION OF THE PROLINE RESIDUE OF
CC PRISTINAMYCIN IIB (PIIB) TO PRISTINAMYCIN IIA (PIIA).
CC -!- COFACTOR: FMN.
CC -!- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SNAI AND SNAB.
CC -!- SIMILARITY: BELONGS TO THE NTAA/SNAA/SOXA(DSZA) FAMILY OF
CC MONOOXYGENASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U21215; AAA83563.1; -
CC Oxidoreductase; Monooxygenase; Flavoprotein; FMN.
CC INIT.MET 0
CC SEQUENCE 421 AA; 46373 MW; 341AD008A939CEFA CRC64;
CC -----
Query Match 93.38; Score 28; DB 1; Length 421;
Best Local Similarity 83.38; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 plglar 6
Db 187 PIGIAR 192
RESULT 9
ID CPA3_RAT STANDARD; PRT; 494 AA.
AC P20812;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 2A3 (EC 1.14.14.1) (CYP2A3) (COUMARIN 7-HYDROXYLASE).
GN CYP2A3 OR CYP2A-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Lung;
RX MEDLINE=90356430; PubMed=2388852;
RA Ueno T., Gonzalez F.;
RT "Complete sequence of the rat CYP2A3 gene specifically transcribed in
RT lung.";
RL Nucleic Acids Res. 18:4623-4624(1990).
RN [2]
RP SEQUENCE OF 8-494 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=89323084; PubMed=2751996;
RA Kimura S., Kozak C.A., Gonzalez F.J.;
RT "Identification of a novel P450 expressed in rat lung: cDNA cloning
RT and sequence, chromosome mapping, and induction by
RT 3-methylcholanthrene.";
RL Biochemistry 28:3798-3803(1989).
CC -!- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
CC MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
CC NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
CC OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
CC ACIDS, AND XENOBIOTICS.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: LUNG.
CC -!- INDUCTION: BY 3-METHYLCHOLANTHRENE (3MC).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC -----

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: M33190; AAA41022.1; -;
 DR EMBL: J02852; AAA88511.1; -;
 DR PIR: A32030; A32030.
 DR PIR: S15056; S15056.
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PRINTS: PR00463; EP4501.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT BINDING 439 439 HEME.
 FT CONFLICT 109 109 W -> G (IN REF. 2).
 FT CONFLICT 335 335 I -> N (IN REF. 2).
 SQ SEQUENCE 494 AA; 56510 MW; F71855CBE602672F CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
 DB 367 PMGLAR 372

RESULT 10
 CP44_MOUSE STANDARD; PRT; 494 AA.
 AC P15392;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CYTOCHROME P450 2M4 (EC 1.14.14.1) (CYPIIA4) (TESTOSTERONE 15-ALPHA-
 DE HYDROXYLASE) (P450-15-ALPHA) (P450-1IA3.1).
 GN CYP2A4 OR CYP2A4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RX MEDLINE=89197954; PubMed=2703500;
 RA Lindberg R., Burkhardt B., Ichikawa T., Negishi M.;
 RT "The structure and characterization of type I P-450(15) alpha gene as
 RT major steroid 15 alpha-hydroxylase and its comparison with type II p-
 RT 450(15) alpha gene.";
 RL J. Biol. Chem. 264:6465-6471(1989).
 RN [2]
 RN SEQUENCE FROM N.A.

RP MEDLINE=88153731; PubMed=3346244;
 RX Squires E.J., Negishi M.;
 RA "Reciprocal regulation of sex-dependent expression of testosterone 15
 RT alpha-hydroxylase (P-450(15 alpha)) in liver and kidney of male mice
 RT by androgen. Evidence for a single gene.";
 RL J. Biol. Chem. 263:4166-4171(1988).
 RN [3]
 RN MUTAGENESIS.
 RP MEDLINE=89281737; PubMed=2733794;
 RX Lindberg R., Negishi M.;
 RA "Alteration of mouse cytochrome P450coh substrate specificity by
 RT mutation of a single amino-acid residue.";
 RL Nature 339:632-634(1989).
 RN [4]

RP TISSUE SPECIFICITY.
 RX MEDLINE=99421934; PubMed=10490589;
 RA Lavery D.J., Lopez-Molina L., Margueron R., Fleury-Olela F.,
 RA Conquet F., Schibler U., Bonfills C.;
 RT "Circadian expression of the steroid 15 alpha-hydroxylase (Cyp2a4) and
 RT coumarin 7-hydroxylase (Cyp2a5) genes in mouse liver is regulated by
 RT the PAR leucine zipper transcription factor DBP.";
 RL Mol. Cell. Biol. 19:6488-6499(1999).
 CC -!- FUNCTION: HIGHLY ACTIVE IN THE 15-ALPHA-HYDROXYLATION OF
 CC TESTOSTERONE. ALSO ACTIVE IN THE 15-ALPHA-HYDROXYLATION OF
 CC PROGESTERONE AND ANDROSTENEDIONE. LITTLE OR NO ACTIVITY ON
 CC CORTICOSTERONE, PREGNENOLONE, DEHYDROEPIANDROSTERONE, ESTRADIOL OR
 CC ESTRIOL.
 CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) -> ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
 CC -!- TISSUE SPECIFICITY: KIDNEY AND LUNG. EXPRESSED IN LIVER, WITH A
 CC STRONG CIRCADIAN RHYTHMICITY. CIRCADIAN EXPRESSION IS REGULATED BY
 CC DBP.
 CC -!- MISCELLANEOUS: THERE ARE ONLY 11 DIFFERENCES BETWEEN THE SEQUENCE
 CC OF TESTOSTERONE 15-ALPHA-HYDROXYLASE AND THAT OF COUMARIN 7-
 CC HYDROXYLASE. BY SITE-DIRECTED MUTAGENESIS IT HAS BEEN SHOWN THAT
 CC MODIFICATION OF POSITION 209 IS SUFFICIENT TO CONVERT THE
 CC SPECIFICITY OF THE TWO FORMS OF THE ENZYME.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: M26208; AAA37797.1; -;
 DR EMBL: M25146; AAA37797.1; JOINED.
 DR EMBL: M25147; AAA37797.1; JOINED.
 DR EMBL: M26202; AAA37797.1; JOINED.
 DR EMBL: M26203; AAA37797.1; JOINED.
 DR EMBL: M26205; AAA37797.1; JOINED.
 DR EMBL: M26206; AAA37797.1; JOINED.
 DR EMBL: M26207; AAA37797.1; JOINED.
 DR EMBL: J03549; AAA40426.1; -;
 DR EMBL: M19319; AAA40429.1; -;
 DR PIR: A33531; A33531.
 DR MGD: MGI:88596; Cyp2a4.
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; p450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 DR PROSITE: PS00463; EP4501.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KW Microsome; Endoplasmic reticulum.
 FT BINDING 439 439 HEME.
 FT CONFLICT 296 296 L -> Q (IN REF. 2).
 FT CONFLICT 306 306 V -> G (IN REF. 2).
 SQ SEQUENCE 494 AA; 56594 MW; 69724BDE3195D75C CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
 DB 367 PMGLAR 372

RESULT 11
 CP45_MOUSE STANDARD; PRT; 494 AA.
 ID CP45_MOUSE
 AC P20852;
 DT 01-FEB-1991 (Rel. 17, Created)

01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYTOCHROME P450 2A5 (EC 1.14.14.1) (CYPIA5) (COUMARIN 7-HYDROXYLASE)
(P450-15-COH) (P450-IIA3.2).
CYP2A5 OR CYP2A-5.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Kidney;
RX MEDLINE=89197954; PubMed=2703500;
RA Lindberg R., Burkhardt B., Ichikawa T., Negishi M.;
RT "The structure and characterization of type I p-450(15) alpha gene as
RT major steroid 15 alpha-hydroxylase and its comparison with type II p-
RT 450(15) alpha gene";
RL J. Biol. Chem. 264:6465-6471(1989).
[2]
SEQUENCE FROM N.A.
RP STRAIN=17NC/Z;
RA Jounaidi Y.;
RT "cDNA and amino acid sequence of a new cyp2a isoform overexpressed in
RT chemically induced mouse hepatoma";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[3]
MUTAGENESIS.
RX MEDLINE=89281737; PubMed=2733794;
RA Lindberg R., Negishi M.;
RT "Alteration of mouse cytochrome P450c10 substrate specificity by
RT mutation of a single amino-acid residue";
RL Nature 339:632-634(1989).
[4]
TISSUE SPECIFICITY.
RX MEDLINE=99421934; PubMed=10490589;
RA Lavery D.J., Lopez-Molina L., Margueron R., Fleury-Olela F.,
RA Conquet F., Schibler U., Bonfils C.;
RT "Circadian expression of the steroid 15 alpha-hydroxylase (Cyp2a4) and
RT coumarin 7-hydroxylase (Cyp2a5) genes in mouse liver is regulated by
RT the PAR leucine zipper transcription factor DBP";
RL Mol. Cell. Biol. 19:6488-6499(1999).
CC -!- FUNCTION: EXHIBITS A HIGH COUMARIN 7-HYDROXYLASE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: LIVER, WITH A STRONG CIRCADIAN RHYTHMICITY.
CC CIRCADIAN EXPRESSION IS REGULATED BY DBP.
CC -!- DEVELOPMENTAL STAGE: IN LIVER; ACTIVITY 6 FOLD HIGHER IN FEMALES
CC THAN IN MALES.
CC -!- MISCELLANEOUS: THERE ARE ONLY 11 DIFFERENCES BETWEEN THE SEQUENCE
CC OF TESTOSTERONE 15-ALPHA-HYDROXYLASE AND THAT OF COUMARIN 7-
CC HYDROXYLASE. BY SITE-DIRECTED MUTAGENESIS IT HAS BEEN SHOWN THAT
CC MODIFICATION OF POSITION 209 IS SUFFICIENT TO CONVERT THE
CC SPECIFICITY OF THE TWO FORMS OF THE ENZYME.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; M25211; AAA37798.1; -
EMBL; M26204; AAA37798.1; JOINED.
DR EMBL; M25205; AAA37798.1; JOINED.
DR EMBL; M25206; AAA37798.1; JOINED.
DR EMBL; M25207; AAA37798.1; JOINED.
DR EMBL; M25208; AAA37798.1; JOINED.
DR EMBL; M25209; AAA37798.1; JOINED.
DR EMBL; M25210; AAA37798.1; JOINED.
DR EMBL; X89864; CAA61963.1; -

PIR; B33531; B33531.
MGD; MGI:88597; Cyp2a5.
InterPro: IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00463; EP450I.
PROSITE; PS00086; CYTOCHROME_P450; 1.
OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 439 439 HEME.
SQ SEQUENCE 494 AA; 56740 MW; 1C2516D5FA2551D0 CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 367 PMGLAR 372

RESULT 12
CPAB_RABIT
ID CPAB_RABIT STANDARD; PRT; 494 AA.
AC Q05556;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CYTOCHROME P450 2A11 (EC 1.14.14.1) (CYP11A1) (P450-IIA11).
GN CYP2A11.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=NEW ZEALAND WHITE; TISSUE=Nasal mucosa;
RX MEDLINE=93352510; PubMed=8349611;
RA Peng H.M., Ding X., Coon M.J.;
RT "Isolation and heterologous expression of cloned cDNAs for two rabbit
RT nasal microsomal proteins, CYP2A10 and CYP2A11, that are related to
RT nasal microsomal cytochrome P450 form a.";
RL J. Biol. Chem. 268:17253-17260(1993).
CC -!- FUNCTION: CATALYZES THE OXYGENATION OF A VARIETY OF SUBSTRATES,
CC INCLUDING ETHANOL AND PROCARINOLENS SUCH AS N-NITROSODIETHYLAMINE
CC AND PHENACETIN. HAS NO OR LITTLE ACTIVITY AS A COUMARIN 7-
CC HYDROXYLASE.
CC -!- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
CC OXIDIZED FLAVOPROTEIN + H(2)O.
CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER AND LUNG AS WELL AS IN
CC NASAL TISSUES.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
or send an email to license@isb-sib.ch).

EMBL; L10237; AAA31372.1; -
DR InterPro: IPR001128; Cyt_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PRINTS; PR00463; EP450I.
PROSITE; PS00086; CYTOCHROME_P450; 1.
OXidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
KW Microsome; Endoplasmic reticulum.
FT BINDING 439 439 HEME (BY SIMILARITY).
SQ SEQUENCE 494 AA; 57277 MW; 28D2E5C4E5D0861A CRC64;

Query Match 93.3%; Score 28; DB 1; Length 494;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 Db 367 PWGLAR 372

RESULT 13
 PROB_MYCTU STANDARD; PRT; 376 AA.
 AC P71910;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK).
 GN PROB OR RV2439C OR MT2515 OR MTCY428.07.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham K., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE -> ADP + L-GLUTAMATE
 CC 5-PHOSPHATE (PRODUCT RAPIDLY CYCLIZES TO 5-OXOPROLINE AND
 CC ORTHOPHOSPHATE).
 CC -!- PATHWAY: FIRST STEP IN PROLINE BIOSYNTHESIS PATHWAY.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE GLUTAMATE 5-KINASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z81451; CAB03780.1; -;
 CC TIGR; MT2515; -;
 CC TubercuList; RV2439c; -;
 CC InterPro; IPR001048; Aakinas.
 CC InterPro; IPR001057; Glut_5_kinase.
 CC InterPro; IPR002478; PUA.
 CC Pfam; PF00696; aakinas; 1.

DR Pfam; PF01472; PUA; 1.
 DR PRINTS; SM00359; PUA; 1.
 DR SMART; SM00359; PUA; 1.
 DR PROSITE; PS00902; GLUTAMATE_5_KINASE; 1.
 KW Transferase; Kinase; Proline biosynthesis; Complete proteome.
 FT CONFLICT 226 226 A -> S (IN REF. 2).
 SQ SEQUENCE 376 AA; 38788 MW; AC7BB66C0B302E6A CRC64;

Query Match 90.0%; Score 27; DB 1; Length 376;
 Best Local Similarity 83.3%; Pred. No. 88;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 Db 67 PLGLSR 72

RESULT 14
 DXS_STRC1 STANDARD; PRT; 631 AA.
 ID DXS_STRC1
 AC Q9REN6;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 1-DEOXY-D-XYLULOSE 5-PHOSPHATE SYNTHASE (EC 2.2.-.-) (1-DEOXYXYLULOSE-
 DE 5-PHOSPHATE SYNTHASE) (DXP SYNTHASE) (DXPS).
 GN DXS.
 OS Streptomyces sp. (strain CL190).
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=93372;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=20115529; PubMed=10648511;
 RA Kuzuyama T., Takagi M., Takahashi S., Seto H.;
 RT "Cloning and characterization of 1-deoxy-D-xylulose 5-phosphate
 RT synthase from Streptomyces sp. Strain CL190, which uses both the
 RT mevalonate and nonmevalonate pathways for isopentenyl diphosphate
 RT biosynthesis.";
 RL J. Bacteriol. 182:891-897(2000).
 CC -!- FUNCTION: CATALYZES THE ACYLOIN CONDENSATION REACTION BETWEEN C
 CC ATOMS 2 AND 3 OF PYRUVATE AND GLYCERALDEHYDE 3-PHOSPHATE TO YIELD
 CC 1-DEOXY-D-XYLULOSE-5-PHOSPHATE (DXP).
 CC -!- PATHWAY: THIAMINE PYROPHOSPHATE. REQUIRES MANGANESE OR MAGNESIUM.
 CC -!- COFACTOR: DEOXYXYLULOSE-5-PHOSPHATE PATHWAY (DXP) OF ISOPRENOID
 CC BIOSYNTHESIS: FIRST STEP. BIOSYNTHETIC PATHWAY TO THIAMINE AND
 CC PYRIDOXOL; FIRST STEP.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- MISCELLANEOUS: OPTIMAL TEMPERATURE IS 42-44 DEGREES CELSIUS AND
 CC OPTIMAL PH IS 9.0.
 CC -!- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY. DXS SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB026631; BAA85847.1; -;
 CC InterPro; IPR000360; Transketolase.
 CC PROSITE; PS00801; TRANSKETOLASE_1; 1.
 CC PROSITE; PS00802; TRANSKETOLASE_2; FALSE_NEG.
 KW Transferase; Flavoprotein; Thiamine pyrophosphate;
 KW Isoprene biosynthesis; Thiamine biosynthesis; Manganese; Magnesium.
 SQ SEQUENCE 631 AA; 67961 MW; 306042CDFA287694 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 631;
 Best Local Similarity 83.3%; Pred. No. 14e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 28, 2002, 16:50:30
Job time: 185 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:05 ; Search time 22.98 Seconds
(without alignments)
38.191 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	%	Length	ID	Description
1	30	100.0	103	2	P72389	P72389 streptomyce
2	30	100.0	193	6	O97940	O97940 sus scrofa
3	30	100.0	351	12	O9J7D9	O9J7D9 bovine para
4	30	100.0	351	12	O9J7D3	O9J7D3 bovine para
5	30	100.0	401	4	O9NT09	O9NT09 homo sapien
6	30	100.0	430	4	O9ULP6	O9ULP6 homo sapien
7	30	100.0	469	4	O9NVE1	O9NVE1 homo sapien
8	30	100.0	484	4	O9NVU9	O9NVU9 homo sapien
9	30	100.0	489	11	O9D1E5	O9D1E5 mus musculus
10	30	100.0	523	2	P96159	P96159 vibrio furn
11	30	100.0	549	2	O9RL52	O9RL52 streptomyce
12	30	100.0	1009	2	O9RUG9	O9RUG9 deinococcus
13	30	100.0	1661	6	O9GKPI	O9GKPI sus scrofa
14	28	93.3	104	11	O9D1S5	O9D1S5 mus musculus
15	28	93.3	230	2	O9HU29	O9HU29 pseudomonas
16	28	93.3	285	10	O40259	O40259 mesembryant
17	28	93.3	491	2	O9A7T1	O9A7T1 caulobacter
18	28	93.3	494	11	O9QZ50	O9QZ50 mesocricetu
19	28	93.3	527	2	O911Q0	O911Q0 pseudomonas

20 28 93.3 708 4 Q9UGU9
21 28 93.3 861 12 O90599
22 28 93.3 941 3 O9C2P5
23 28 93.3 1353 4 O9Y6Y1
24 27 90.0 65 4 Q9UH04
25 27 90.0 100 11 Q9CUD1
26 27 90.0 114 12 Q9DW90
27 27 90.0 132 2 O86523
28 27 90.0 175 1 Q9YDM6
29 27 90.0 185 10 Q38688
30 27 90.0 190 2 O86520
31 27 90.0 192 12 O55942
32 27 90.0 202 1 Q9HPR0
33 27 90.0 213 2 P73135
34 27 90.0 227 10 Q9FEM1
35 27 90.0 256 10 Q9XF85
36 27 90.0 286 10 Q9C639
37 27 90.0 280 10 Q9XF89
38 27 90.0 286 10 Q00321
39 27 90.0 302 10 Q41040
40 27 90.0 360 2 O9A2D1
41 27 90.0 379 2 O9JRB5
42 27 90.0 429 10 Q9LIT6
43 27 90.0 443 4 Q9UEW4
44 27 90.0 479 10 Q9M903
45 27 90.0 660 2 O69710

ALIGNMENTS

RESULT 1
P72389 ID P72389 PRELIMINARY; PRT; 103 AA.
AC P72389;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HISTIDINE KINASE HOMOLOG (ABSA1) AND RESPONSE REGULATOR HOMOLOG
DE (ABSA2) GENES, COMPLETE CDS (FRAGMENT).
D7.
GN Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J1501;
RX MEDLINE=96236039; PubMed=8655502;
RA Brian P., Riggie P.J., Santos R.A., Champness W.C.;
RT "Global negative regulation of Streptomyces coelicolor antibiotic
RT synthesis mediated by an absA-encoded putative signal transduction
RT system";
RL J. Bacteriol. 178:3221-3231(1996).
DR EMBL; U51332; AAB08051.1; -
DR InterPro; IPR001687; ATP_GTP_A.
FT NON_TER 103
SQ SEQUENCE 103 AA; 10989 MW; BA0C3C8424268398 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 94 PLGLAR 99

RESULT 2
O97940 ID O97940 PRELIMINARY; PRT; 193 AA.
AC O97940

```

Query Match      100.0%; Score 30; DB 12; Length 351;
Best Local Similarity 100.0%; Pred. NO. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      T g l g l a r 6
        | | | | |

```

```

Query Match      100.0%; Score 30; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 plglar 6
        | | | | |
Db      126 PLGLAR 131

RESULT      6

```

```
Q9ULP6          PRELIMINARY;          PRT;      430 AA.
ID Q9ULP6;
AC Q9ULP6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE KIAA1174 PROTEIN (FRAGMENT).
GN KIAA1174.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
DR EMBL; AB033000; BAA86488.1; -.
FT NON_TER
SQ SEQUENCE 430 AA; 48405 MW; 684C67BD3F60DFD1D CRC64;

Query Match          100.0%; Score 30; DB 4; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 251 PLGLAR 256

RESULT 7
Q9NVE1          PRELIMINARY;          PRT;      469 AA.
ID Q9NVE1;
AC Q9NVE1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CDNA FLJ10789 FIS, CLONE NT2RP4000500.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
RA Matsunura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001651; BA91811.1; -.
SQ SEQUENCE 469 AA; 53215 MW; 181059F23AD87DF5 CRC64;

Query Match          100.0%; Score 30; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 214 PLGLAR 219

RESULT 8
Q9NVU9          PRELIMINARY;          PRT;      484 AA.
ID Q9NVU9;
AC Q9NVU9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
```

```
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE CDNA FLJ10494 FIS, CLONE NT2RP2000283.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isoqai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Niimiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK001356; BAA91646.1; -.
SQ SEQUENCE 484 AA; 53901 MW; C309EED810F4796A CRC64;

Query Match          100.0%; Score 30; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
DB 209 PLGLAR 214

RESULT 9
Q9DIE5          PRELIMINARY;          PRT;      489 AA.
ID Q9DIE5;
AC Q9DIE5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 1110013E13RIK PROTEIN.
GN 1110013E13RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003656; BAB22919.1; -.
DR MGD; MGI:1922025; 1110013E13RIK.
SQ SEQUENCE 489 AA; 54957 MW; 50AA85EF2C58B79A CRC64;
```

Query Match 100.0%; Score 30; DB 11; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 plglar 6
DB 214 PLGLAR 219

RESULT 10

P6159 ID P6159 PRELIMINARY; PRT; 523 AA.
AC P6159;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PTS PERMEASE FOR GLUCOSE.
GN MALX.
OS Vibrio furnissii.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=29494;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SR1514.
RX MEDLINE=97125987; PubMed=8969209;
RA Bouma C.L., Roseman S.;
RT "Sugar transport by the marine chitinolytic bacterium Vibrio furnissii. Molecular cloning and analysis of the glucose and N-acetylglucosamine permeases.";
RL J. Biol. Chem. 271:33457-33467(1996).
DR EMBL; U65013; AAC44676.1; -.
DR HSSP; P05053; IIBA.
DR InterPro; IPR001996; PTS_EIIB.
DR InterPro; IPR003352; PTS_EIIC.
DR Pfam; PF00367; PTS_EIIB; 1.
DR Pfam; PF02378; PTS_EIIC; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
SQ SEQUENCE 523 AA; 55932 MW; 90D03CD004A3FE48 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 plglar 6
DB 84 PLGLAR 89

RESULT 11

Q9RL52 ID Q9RL52 PRELIMINARY; PRT; 549 AA.
AC Q9RL52;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SUGAR PHOSPHOTRANSFERASE.
GN MALX.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Murphy L., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kisser H.M., Denapatis D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL; AL121596; CAB56664.1; -.
DR HSSP; P05053; IIBA.
DR InterPro; IPR001996; PTS_EIIB.
DR InterPro; IPR003352; PTS_EIIC.
DR Pfam; PF00367; PTS_EIIB; 1.
DR Pfam; PF02378; PTS_EIIC; 1.
DR PROSITE; PS01035; PTS_EIIB_CYS; 1.
KW Transferase.
SQ SEQUENCE 549 AA; 58601 MW; F4750674A78D850A CRC64;

Query Match 100.0%; Score 30; DB 2; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 plglar 6
DB 83 PLGLAR 88

RESULT 12

Q9RUG9 ID Q9RUG9 PRELIMINARY; PRT; 1009 AA.
AC Q9RUG9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PENICILLIN-BINDING PROTEIN 1B MCRB, PUTATIVE.
GN DR1417.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001986; AAF10981.1; -.
DR TIGR; DR1417; -.
DR InterPro; IPR001264; Transglycosyl.
DR InterPro; IPR001460; Transpeptidase.
DR Pfam; PF00912; Transglycosyl; 1.
DR Pfam; PF00905; Transpeptidase; 1.
DR ProDom; PD001895; Transglycosyl; 1.
KW Complete proteome.
SQ SEQUENCE 1009 AA; 111165 MW; 4B9A9508C5E52B72 CRC64;

Query Match 100.0%; Score 30; DB 2; Length 1009;
Best Local Similarity 100.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 plglar 6
DB 121 PLGLAR 126

RESULT 13
Q9GKPI PRELIMINARY; PRT; 1661 AA.
AC Q9GKPI; 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE COMPLEMENT COMPONENT C3.
GN C3.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Wimmers K., Ponsuksilli S., Schmolli F., Schellander K.;
RT "Molecular genetic analysis of the porcine C3 gene.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154933; AAG40565.1; -;
DR InterPro; IPR002890; A2M_N.
DR InterPro; IPR001599; Alpha_2_macrogloblIn.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR001840; Anaphylatoxin.
DR InterPro; IPR001134; Netrin_C.
DR Pfam; PF00207; A2M; 1.
DR Pfam; PF01835; A2M_N; 1.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF01759; NTR; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
DR ProDom; PD003264; Anaphylatoxin; 1.
DR SMART; SM00104; ANATO; 1.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
SQ SEQUENCE 1661 AA; 186806 MW; 4899D0914BE3310C CRC64;

Query Match 100.0%; Score 30; DB 6; Length 1661;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 741 PLGLAR 746

RESULT 14
Q9D1S5 PRELIMINARY; PRT; 104 AA.
AC Q9D1S5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1100001D15RIK PROTEIN.
GN 1100001D15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=257BL/6J; TISSUE=EMBRYO;
RX MEDLINE=C1085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003155; BAB22609.1; -;
DR MGD; MGI:1915679; l100001D15RIK.
SQ SEQUENCE 104 AA; 11682 MW; 14EFBF0AEB02A3CC CRC64;

Query Match 93.3%; Score 28; DB 11; Length 104;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 20 PLGLAR 25

RESULT 15
Q9HU29 PRELIMINARY; PRT; 230 AA.
AC Q9HU29;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PROBABLE PERMEASE OF ABC TRANSPORTER.
GN PA5155.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goitry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; AE004928; AAG08540.1; -;
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 1.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 230 AA; 26155 MW; FC9F0CF5DA374316 CRC64;

Query Match 93.3%; Score 28; DB 2; Length 230;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 38 PLGLAR 43

Search completed: February 28, 2002, 16:50:13
Job time: 188 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 : Search time 23.88 Seconds
(without alignments)
18.611 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_1101.*
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	30	100.0	6	18	3-methylcholanthrene
2	30	100.0	6	19	Matrix metallopro
3	30	100.0	8	5	Sequence of peptid
4	30	100.0	77	22	Pig C3a anaphylato
5	30	100.0	103	20	N-terminal fragmen
6	30	100.0	351	11	Viral membrane pro
7	30	100.0	362	22	Human secreted pro
8	30	100.0	469	22	Human polypeptide
9	30	100.0	469	22	Human protein sequ
10	30	100.0	484	22	Human protein sequ
11	30	100.0	489	21	Amino acid sequenc

12	30	100.0	489	21	AAV66660	Membrane-bound pro
13	30	100.0	489	22	AAV38703	Human polypeptide
14	30	100.0	489	22	AAV65183	Human PRO783 (UNQ4
15	30	100.0	538	22	AAV40489	Human polypeptide
16	30	100.0	538	22	AAV40490	Human polypeptide
17	30	100.0	1061	20	AAV87504	Human N-methyl-D-a
18	30	100.0	1081	21	AAV26240	Human N-methyl-D-a
19	30	100.0	1212	20	AAV87503	Human N-methyl-D-a
20	30	100.0	1232	21	AAV26239	Human N-methyl-D-a
21	28	93.3	422	15	AAV54202	snah gene product
22	27	90.0	134	22	AAU04893	Micromonospora eve
23	27	90.0	159	21	AAV26215	Arabidopsis thalia
24	27	90.0	159	21	AAV26215	Arabidopsis thalia
25	27	90.0	161	21	AAV28187	Arabidopsis thalia
26	27	90.0	217	22	AAV3531	Human protein sequ
27	27	90.0	224	20	AAV74086	Human prostate tum
28	27	90.0	230	22	AAV95751	Human protein sequ
29	27	90.0	256	21	AAV28186	Arabidopsis thalia
30	27	90.0	265	21	AAV28185	Arabidopsis thalia
31	27	90.0	272	21	AAV26214	Arabidopsis thalia
32	27	90.0	272	21	AAV2745	Arabidopsis thalia
33	27	90.0	275	19	AAV48847	Rat receptor tyros
34	27	90.0	280	21	AAV26213	Arabidopsis thalia
35	27	90.0	280	21	AAV2744	Arabidopsis thalia
36	27	90.0	376	22	AAV81188	Mycobacterium tube
37	27	90.0	404	21	AAV58135	Arabidopsis thalia
38	27	90.0	417	21	AAV58134	Arabidopsis thalia
39	27	90.0	419	21	AAV58133	Arabidopsis thalia
40	27	90.0	460	22	AAV91347	C glutamicum prote
41	27	90.0	472	19	AAV48848	Human receptor tyr
42	27	90.0	604	18	AAV42400	Partial sequence o
43	27	90.0	745	22	AAV67331	Human neuron proge
44	26	86.7	46	22	AAV63399	Human breast cance
45	26	86.7	48	21	AAV65041	Human 5' EST relat

ALIGNMENTS

RESULT 1
AAB74602
ID AAB74602 standard; peptide; 6 AA.
XX
AC AAB74602;
DT 21-MAY-2001 (first entry)
XX
DE 3-methylcholanthrene (MCA) peptide substrate.
XX
KW 3-methylcholanthrene; MCA; substrate; metalloproteinase inhibitor;
KW cancer; metastasis; arthritis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Pro in N-terminally modified to
FT FT 7-methoxycoumarin-4-yl-acetyl-pro"
FT Modified-site 5 /note= "Ala is N-terminally modified to
FT FT 3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl-ala"
FT Modified-site 6 /note= "amidated"
FT FT
FT FT
XX WO9720824-A1.
XX
XX
PD 12-JUN-1997
XX
XX
PF 05-DEC-1996; 96WO-US19328.
XX
XX
PR 08-DEC-1995; 95US-0569766.
XX
XX
PA (AGOU-) AGOURON PHARM INC.

XX Zook SE, Dagnino R, Deason ME, Bender SL, Melnick MJ;
 XX WPI; 1997-332465/30.
 XX
 XX New N-hydroxy-benzenesulphonyl carboxamide derivatives - are
 PT metallo-protease inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 XX Example 22; Page 108; 151pp; English.
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. N-hydroxy benzenesulphonyl (thiazine or piperazine)
 CC carboxamide derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 2
 AAWS2139
 ID AAWS2139 standard; Peptide; 6 AA.
 XX
 AC AAWS2139;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Matrix metalloproteinase MMP-9 substrate B.
 XX
 KW Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;
 KW matrix metalloproteinase 12; MMP-12; osteoclastic proteinase;
 KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;
 KW bone resorption; metastasis; tumour; cancer; ulcer; arthritis;
 KW periodontal disease; therapy.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Mca-proline"
 FT Cleavage-site 3..4
 FT Modified-site 5
 FT /note= "Dpa-alanine"
 XX
 FT WO9804287-A1.
 PN
 XX
 XX 05-FEB-1998.
 PD
 XX
 XX 29-JUL-1997; 97WO-EP04110.
 PF
 XX
 XX 30-JUL-1996; 96GB-0015976.
 PR
 XX (CLIN-) CENT CLINICAL & BASIC RES.
 PA
 XX Delaisse J, Foged NT, Meldal M;
 PI WPI; 1998-130425/12.
 XX
 XX Use of inhibitors of protease(s) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as
 PT osteoporosis
 XX
 XX Example 6b; Page 44; 110pp; English.
 PS
 XX
 CC Peptide B is a substrate of matrix metalloproteinase MMP-9. Novel
 CC peptide substrate mimicking MMP-inhibitors (see AAWS2132-33) are
 CC promising agents for use in treatment of bone metabolic disease.
 CC They can be used to inhibit proteinases involved in the
 CC recruitment, proliferation, differentiation or migration of
 CC osteoclast precursor cells or in the migration, fusion, attachment,
 CC polarisation, removal of mineralised osseous substance or death of
 CC osteoclasts. The inhibitors reduce the rate of bone resorption
 CC and are used to treat or prevent, e.g. osteoporosis and osteolytic
 CC bone metastases. They are also useful in, e.g. treatment of
 CC cancer, ulcers, arthritis and periodontal disease.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 Db | | | | |
 1 piglar 6
 RESULT 3
 AAP40579
 ID AAP40579 standard; peptide; 8 AA.
 XX
 AC AAP40579;
 XX
 DT 13-FEB-1992 (first entry)
 XX
 DE Sequence of peptides which control smooth muscle contraction,
 DE histamine release and vascular permeability.
 XX
 KW Asthma therapy; bronchial allergy; inflammatory response.
 XX
 PN US4438029-A.
 XX
 PD 20-MAR-1984.
 XX
 PF 21-FEB-1979; 79US-0013176.
 XX
 PR 21-FEB-1979; 79US-0013176.
 PR 25-JAN-1977; 77US-0762427.
 PR 19-JAN-1978; 78US-0870713.
 XX
 XX (RESE) RESEARCH CORP.
 XX
 XX Erickson BW, Hugli TE;
 PI WPI; 1984-088186/14.
 DR
 XX
 PT Peptides contg. Gly-Leu-Ala-Arg sequence - useful in promotion or
 PT inhibition of smooth muscle contraction, histamine release and
 PT vascular permeability
 XX
 PS Claim 6; column 7; 5pp; English.
 XX
 CC Gly-Leu-Ala-Arg (I) and peptides contg. (I) with Arg as the carboxyl
 CC terminus, contract smooth muscle, release histamine from mast cells
 CC and enhance vascular permeability. Peptides contg. the unit (I)-Gly
 CC are antagonists of this activity. The peptide with a carboxy
 CC terminus canavanine residue behaves similarly to those with Arg in
 CC this posn. Doses may be up to 2g or more per day, e.g. in units of
 CC 250mg.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 30; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 3 plglar 8

RESULT 4
 AAE05446
 ID AAE05446 standard; Protein: 77 AA.

XX AC AAE05446;

DT 24-SEP-2001 (first entry)

XX DE DE Pig C3a anaphylatoxin.

XX KW Mannan binding protein-associated serine protease; MASP;
 KW complement-activation; C-activation; microbial infection;
 KW cyomegalovirus; CMV; hepatitis virus; human immunodeficiency virus;
 KW HIV; organ transplant rejection; tissue injury; autoimmune disease;
 KW rheumatoid arthritis; systemic lupus erythematosus; SLE;
 KW inflammatory response; Alzheimer's disease; pig; C3a anaphylatoxin.

XX OS Sus scrofa.

XX PN US6235494-B1.

XX PD 22-MAY-2001.

XX PF 08-FEB-1999; 99US-0246500.

XX PR 08-FEB-1999; 99US-0246500.

XX (SCRI) SCRIPPS RES INST.

XX PA Hugli TE;

XX WPI; 2001-450082/48.

XX Method for determining in-vivo levels of activated mannan binding
 PT protein-associated serine protease enzyme, and new peptide derivatives

XX Claim 3; Column 43-44; 39pp; English.

XX The invention relates to assays for measuring in-vivo levels of
 CC activated mannan-binding protein-associated serine protease (MASP-1 and
 CC MASP-2) activity. The assay comprises contacting a sample of blood or
 CC plasma comprising a metal ion chelator with a substrate of formula:
 CC R-peptide-Y; wherein the peptide comprises at least 4 residues from the
 CC C-terminus of an anaphylatoxin selected from C3a, C4a and C5a; R is a
 CC peptide blocking, protecting or capping group; and Y is any group
 CC cleavable from the substrate by MASP and comprises a labelled tag. The
 CC substrate of the invention is also useful for monitoring in vitro and
 CC in vivo complement-activation (C-activation) by classical, alternative
 CC or lectin pathways. The assays of MASP activity can be used for
 CC detecting or monitoring a condition associated with complement
 CC activation. The conditions include microbial infections
 CC caused by particularly cytomegalovirus (CMV), hepatitis virus and
 CC human immunodeficiency virus (HIV), organ transplant rejection, tissue
 CC injury, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE)) and inflammatory responses (e.g. in Alzheimer's
 CC disease and bacterial diseases). The assay of MASP is also useful for
 CC assessing the toxicity or injury of therapeutic treatments or screening
 CC test compounds as agents for treatment of viral diseases, parasitic
 CC infections, tissue injury, organ transplant rejection, autoimmune
 CC diseases or inflammatory responses. The present sequence is pig C3a
 CC anaphylatoxin.

XX SQ Sequence 77 AA;

Query Match 100.0%; Score 30; DB 22; Length 77;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 72 plglar 77

RESULT 5

AAW78493

ID AAW78493 standard; Protein: 103 AA.

XX AC AAW78493;

XX DT 21-MAY-1999 (first entry)

XX DE N-terminal fragment S.coelicolor D7 protein.

XX KW AbsA; operon; open reading frame; histidine kinase; response regulator;
 KW mutation; insertion; antibiotic; actinorhodin; undecylprodigiosin.

XX OS Streptomyces coelicolor.

XX PN US5876987-A.

XX PD 02-MAR-1999.

XX PF 06-FEB-1997; 96US-0796414.

XX PR 07-FEB-1996; 96US-0011286.

XX PR 06-FEB-1997; 97US-0796414.

XX (UNMS) UNIV MICHIGAN STATE.

XX PI Anderson TB, Brian P, Champness WC;

XX WPI; 1999-189640/16.

XX N-PSDB; AAX21397.
 XX Recombinant Streptomyces species - useful for the production of
 PT recombinant proteins and the hyper-expression of antibiotics,
 PT particularly actinorhodin and undecylprodigiosin

XX Disclosure; Fig 4; 30pp; English.

XX The sequences AAX21397-X21399 represent overlapping sequences from the
 CC AbsA operon of Streptomyces coelicolor. This sequence corresponds to
 CC the N-terminal portion of the D7 protein. The invention relates to
 CC the AbsA1 protein (AAW78491) which is a histidine kinase and the related
 CC protein AbsA2 (AAW78492) (also encoded by the operon) which is a
 CC response regulator for the AbsI gene. Inactivation of the AbsI gene
 CC either by mutation or insertion of heterologous DNA into the AbsI gene
 CC results in a Streptomyces organism which can hyperproduce heterologous
 CC proteins or antibiotics, especially actinorhodin and undecylprodigiosin.

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 30; DB 20; Length 103;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
 |||||
 Db 94 plglar 99

RESULT 6

AAR06024
ID AAR06024 standard; protein; 351 AA.

XX AC AAR06024;

DT 04-DEC-1990 (first entry)

XX DE Viral membrane protein.

XX KW Haemagglutinin neuraminidase; vaccine; parainfluenza; ds.

XX OS Bovine parainfluenza type III virus.

XX PN JP02156883-A.

XX PD 15-JUN-1990.

XX PF 09-DEC-1988; 88JP-0311655.

XX PR 09-DEC-1988; 88JP-0311655.

XX PA (JAPG) NIPPON ZEON KK.

XX XX WPI; 1990-228484/30.

DR N-PSDB; AAQ05320.

XX Recombinant vaccinia virus - is which all or part of DNA coding
PT membrane fusion protein in combined to genom region.

XX PS Disclosure; ; p; Japanese.

XX CC Fragment of parainfluenza viral membrane fusion protein encoding DNA
CC may be incorporated into the vaccina virus, which may then be used
CC as a live vaccine for cows.

XX SQ Sequence 351 AA;

Query Match 100.0%; Score 30; DB 11; Length 351;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 piglar 6

DB 93 piglar 98

RESULT 7

AAG89160
ID AAG89160 standard; Protein; 362 AA.

XX AC AAG89160;

DT 11-SEP-2001 (first entry)

XX DE Human secreted protein, SEQ ID NO: 280.

XX KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
KW GENSET.

XX OS Homo sapiens.

XX PN WO200142451-A2.

XX PD 14-JUN-2001.

XX PF 07-DEC-2000; 2000WO-IB01938.

XX XX 08-DEC-1999; 99US-0169629.

PR 06-MAR-2000; 2000US-0187470.

XX XX (GENSET) GENSET.

PI Dumas Milne Edwards J, Bougueleret L, Jobert S;

XX WPI; 2001-367870/38.

DR N-PSDB; AAH64763.

XX Full length GENSET human nucleic acids encoding potentially secreted
PT proteins, useful in gene therapy and vaccination against a variety of
PT diseases, and for diagnosis of those diseases -

XX PS Claim 21; Page 816; 921pp; English.

XX The invention relates to full length GENSET human nucleic acids encoding
CC potentially secreted proteins. The nucleic acids and the polypeptides
CC they encode may be used in the prevention, treatment and diagnosis of
CC diseases associated with inappropriate GENSET gene expression. For
CC example, they be used to treat disorders associated with decreased
CC GENSET gene expression by rectifying mutations or deletions in a
CC patient's genome that affect the activity of GENSET or by supplementing
CC the patients own production of GENSET polypeptides. Conversely,
CC antisense nucleic acid molecules may be administered to down regulate
CC GENSET expression by binding with the cells' own genes and preventing
CC their expression. The sense and antisense nucleic acids may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acid sequences in samples, and hence to
CC determine which patients may be in need of restorative therapy.
CC The GENSET polypeptides may be used as antigens in the production of
CC antibodies and in assays to identify modulators (agonists and
CC antagonists) of GENSET polypeptide expression and activity. The
CC present sequence is a GENSET polypeptide of the invention.

XX SQ Sequence 362 AA;

Query Match 100.0%; Score 30; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 piglar 6

DB 87 piglar 92

RESULT 8

AAM38704
ID AAM38704 standard; Protein; 469 AA.

XX AC AAM38704;

XX DT 22-OCT-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 1849.

XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW Leukaemia.

XX OS Homo sapiens.

XX PN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US34263.

XX PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 XX WPI: 2001-442253/47.
 DR N-PSDB; AA157860.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Example 3; SEQ ID NO 1849; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA138642-AA142213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 XX Sequence 469 AA;
 SQ

Query Match 100.0%; Score 30; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 |||||
 Db 214 plglar 219

RESULT 9
 AAB93173
 ID AAB93173 standard; Protein; 469 AA.
 AC
 AC AAB93173;
 XX
 XX 26-JUN-2001 (first entry)
 DT
 XX
 XX Human protein sequence SEQ ID NO:12110.
 DE
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 PR
 XX (HELI-) HELIX RES INST.
 PA

XX
 PI Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 XX WPI: 2001-318749/34.
 DR
 XX
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX
 PS Claim 8; SEQ ID 12110; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 XX Sequence 469 AA;
 SQ

Query Match 100.0%; Score 30; DB 22; Length 469;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
 |||||
 Db 214 plglar 219

RESULT 10
 AAB92882
 ID AAB92882 standard; Protein; 484 AA.
 AC
 AC AAB92882;
 XX
 XX 26-JUN-2001 (first entry)
 DT
 XX
 XX Human protein sequence SEQ ID NO:11481.
 DE
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP1074617-A2.
 PN
 XX 07-FEB-2001.
 PD
 XX 28-JUL-2000; 2000EP-0116126.
 PF
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 PR
 XX (HELI-) HELIX RES INST.
 PA

XX (HELI-) HELIX RES INST.
PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
DR
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX Claim 8; SEQ ID 11481; 2537pp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
XX Sequence 484 AA:
XX
XX Query Match 100.0%; Score 30; DB 22; Length 484;
XX Best Local Similarity 100.0%; Pred. No. 62;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 p1qlar 6
XX |111111
XX Db 209 p1qlar 214
XX
XX
XX RESULT 11
XX AAB18971
XX ID AAB18971 standard; Protein; 489 AA.
XX
XX AC AAB18971;
XX
XX DT 08-FEB-2001 (first entry)
XX
XX DE Amino acid sequence of a human transmembrane protein.
XX
XX KW Human; transmembrane protein; cell proliferation disorder; myeloma;
XX reproductive disorder; smooth muscle disorder; neurological disorder;
XX arteriosclerosis; leukaemia; acquired immunodeficiency syndrome; AIDS;
XX allergy; ovulatory defect; angina; hypertension; stroke; epilepsy;
XX Alzheimer's disease; Tourette's disorder.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Modified-site 10
XX FT /note= "potential phosphorylation site"
XX FT Modified-site 51
XX FT /note= "potential phosphorylation site"

FT Modified-site 52
FT /note= "potential phosphorylation site"
FT Modified-site 105
FT /note= "potential glycosylation site"
FT Modified-site 121
FT /note= "potential glycosylation site"
FT Modified-site 135
FT /note= "potential phosphorylation site"
FT Modified-site 143
FT /note= "potential phosphorylation site"
FT Modified-site 185
FT /note= "potential phosphorylation site"
FT Modified-site 224
FT /note= "potential phosphorylation site"
FT Modified-site 244
FT /note= "potential phosphorylation site"
FT Modified-site 252
FT /note= "potential phosphorylation site"
FT Region 263..284
FT /note= "leucine zipper"
FT Modified-site 279
FT /note= "potential phosphorylation site"
FT Modified-site 291
FT /note= "potential phosphorylation site"
FT Modified-site 379
FT /note= "potential phosphorylation site"
FT Region 399..420
FT /note= "leucine zipper"
FT Modified-site 416
FT /note= "potential phosphorylation site"
FT Modified-site 483
FT /note= "potential phosphorylation site"
XX WO200056891-A2.
XX
XX PD 28-SEP-2000.
XX
XX PF 22-MAR-2000; 2000WO-US07817.
XX
XX PR 22-MAR-1999; 99US-0125537.
XX PR 16-JUN-1999; 99US-0139565.
XX
XX PA (INCY-) INCYTE PHARM INC.
XX
XX PI Yue H, Lal P, Tang YT, Hillman JL, Reddy R, Bandman O, Baughn MR;
XX Lu DAM, Azimzai Y, Yang J;
XX
XX DR WPI; 2000-579485/54.
XX DR N-PSDB; AAA96484.
XX
XX PT New human transmembrane proteins are used to treat a disease or
XX condition associated with decreased expression of functional HTMP e.g.
XX Tourette's disorder, angina and leukaemia -
XX
XX PS Claim 1; Page 92-93; 130pp; English.
XX
XX CC The present sequence represents a human transmembrane proteins (HTMP).
XX Agonists and antagonists of the protein are used to treat a disease
XX or condition associated with overexpression of the protein. Diseases
XX and conditions which can be treated include cell proliferative,
XX immunological, reproductive, smooth muscle and neurological disorders
XX e.g. arteriosclerosis, myeloma, leukaemia, acquired immunodeficiency
XX syndrome (AIDS), allergies, ovulatory defects, angina, hypertension,
XX stroke, Alzheimer's disease, epilepsy and Tourette's disorder. The
XX polynucleotides may be used to detect and quantify gene expression in
XX biopsied tissues where protein expression may be correlated with disease
XX e.g. to determine absence, presence or excess expression of HTMP or to
XX monitor regulation of HTMP expression during therapeutic intervention.
XX
XX SQ Sequence 489 AA;

Query Match 100.0%; Score 30; DB 21; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 214 plglar 219

RESULT 12
AAY66660
ID AAY66660 standard; protein; 489 AA.
XX AC AAY66660;
XX DT 05-APR-2000 (first entry)
XX DE Membrane-bound protein PRO783.
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX KW pharmaceutical; receptor immunoadhesin; gene mapping.
XX OS Homo sapiens.
XX PN WO9963088-A2.
XX PD 09-DEC-1999.
XX PF 02-JUN-1999; 99WO-US12252.
XX PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.

PR 18-AUG-1998; 98US-0096959.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 XX

PA (GETH) GENENTECH INC.

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
 PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.

DR N-PSDB; AA264989.

XX Membrane-bound proteins and related nucleotide sequences

PT claim 12; Fig 79; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.

XX Sequence 489 AA;

Query Match 100.0%; Score 30; DB 21; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6

|||||

Db 214 plglar 219

RESULT 13

AAM38703

ID AAM38703 standard; Protein; 489 AA.

XX AAM38703;

AC AAM38703;

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 1848.

DE

XX

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX PA

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI57859.

XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX Example 3; SEQ ID NO 1848; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: Immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 489 AA;

QY 1 plglar 6

|||||

Db 214 plglar 219

Query Match 100.0%; Score 30; DB 22; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6

|||||

Db 214 plglar 219

RESULT 14

AAB65183

ID AAB65183 standard; Protein; 489 AA.

XX AAB65183;

AC AAB65183;

DT 02-APR-2001 (first entry)

XX Human PRO783 (UNQ458) protein sequence SEQ ID NO:138.

DE

XX

KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.

OS Homo sapiens.

XX WO200073454-A1.

PN 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 08-OCT-1999; 99US-0158663.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 02-MAR-2000; 2000WO-US05004.

PR 15-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US06884.

XX 20-MAR-2000; 2000WO-US07377.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Fong S, Gerber H, Grietsen ME, Goddard A, Godowski PJ;

PI Grimaldi CJ, Gurney AL, Kijavlin IL, Napier MA, Pan J, Paoni NF;

PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

PI Zhang Z;

XX WPI; 2001-032160/04.

XX N-PSDB; AAF44135.

XX PRO polynucleotides used to produce polypeptides used to target

PT bioactive molecules such as toxins, radiolabels or antibodies, to

PT specific cells, to cause targeted cell death -

XX Claim 12; Fig 79; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

CC proteins. The PRO proteins have cytostatic activity. The PRO proteins

CC can be used for targeted delivery of bioactive molecules, such as

CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide

CC sequences, and their fragments, can be used as hybridisation probes, in

CC chromosomal and gene mapping, and in the generation of anti-sense RNA

CC and DNA. They may also be used to produce transgenic animals which are

CC used to develop and screen therapeutically useful reagents. The PRO

CC nucleotide and protein sequence can be used for tissue typing and in

CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used

CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and

CC AAF63154 to AAF65300 represent human PRO polynucleotide and protein

CC sequences given in the exemplification of the present invention.

XX Sequence 489 AA;

Query Match

100.0%; Score 30; DB 22; Length 489;

Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglar 6

Db 214 plglar 219

RESULT 15

AAM40489

ID AAM40489 standard; Protein; 538 AA.

XX AAM40489;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 5420.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AAI59645.

XX Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

XX Example 2; SEQ ID NO 5420; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

XX Note: The sequence data for this patent did not form part of the printed
XX specification.

SQ Sequence 538 AA;

Query Match 100.0%; Score 30; DB 22; Length 538;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plqlar 6

Db 281 plqlar 286

Search completed: February 28, 2002, 16:47:04

Job time: 59 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 93.69 Seconds
(without alignments)
17.781 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	30	100.0	6	18	US-09-464-908-1
2	30	100.0	7	19	US-09-588-417-6
3	30	100.0	128	23	US-09-902-540-12523
4	30	100.0	177	21	US-09-758-472-5376
5	30	100.0	203	16	US-09-252-991A-19176
6	30	100.0	230	16	US-09-252-691-6030
7	30	100.0	230	16	US-09-252-691C-6030
8	30	100.0	277	1	PCT-US01-14827-12965
9	30	100.0	293	16	US-09-252-991A-19047

10	30	100.0	333	19	US-09-562-737-6	Sequence 6, Appli
11	30	100.0	362	1	PCT-US01-16450-2736	Sequence 2736, Ap
12	30	100.0	362	1	PCT-US01-16450A-2736	Sequence 2736, Ap
13	30	100.0	362	21	US-09-731-872-280	Sequence 280, App
14	30	100.0	362	22	US-09-876-997-280	Sequence 280, App
15	30	100.0	362	24	US-60-169-629-495	Sequence 495, App
16	30	100.0	362	24	US-60-187-470-495	Sequence 495, App
17	30	100.0	406	23	US-09-902-540-13528	Sequence 13528, A
18	30	100.0	465	18	US-09-488-725A-1849	Sequence 1849, Ap
19	30	100.0	489	16	US-09-252-991A-17683	Sequence 17683, A
20	30	100.0	489	18	US-09-488-725A-1848	Sequence 1848, Ap
21	30	100.0	489	21	US-09-709-238-138	Sequence 138, App
22	30	100.0	489	23	US-09-941-992-138	Sequence 138, App
23	30	100.0	489	24	US-60-125-537-8	Sequence 8, Appli
24	30	100.0	535	18	US-09-489-039A-13906	Sequence 13906, A
25	30	100.0	538	18	US-09-488-725A-5420	Sequence 5420, Ap
26	30	100.0	538	18	US-09-488-725A-5421	Sequence 5421, Ap
27	30	100.0	592	23	US-09-955-999-112	Sequence 112, App
28	30	100.0	635	16	US-09-252-991A-16721	Sequence 16721, A
29	28	93.3	38	7	US-08-344-185C-428	Sequence 428, App
30	28	93.3	38	7	US-08-344-185C-428	Sequence 428, App
31	28	93.3	182	16	US-09-252-691-9747	Sequence 9747, Ap
32	28	93.3	182	16	US-09-252-691C-9747	Sequence 9747, Ap
33	28	93.3	196	16	US-09-252-991A-18189	Sequence 18189, A
34	28	93.3	206	16	US-09-270-767-57749	Sequence 57749, A
35	28	93.3	206	16	US-09-270-849B-182867	Sequence 182867, A
36	28	93.3	273	16	US-09-252-991A-32405	Sequence 32405, A
37	28	93.3	357	16	US-09-270-767-42454	Sequence 42454, A
38	28	93.3	381	16	US-09-252-991A-28320	Sequence 28320, A
39	28	93.3	469	24	US-60-324-109-30092	Sequence 30092, A
40	28	93.3	478	24	US-60-312-544-10512	Sequence 10512, A
41	28	93.3	481	16	US-09-252-991A-23317	Sequence 23317, A
42	28	93.3	494	15	US-09-126-420A-26	Sequence 26, Appl
43	28	93.3	544	17	US-09-328-352-6896	Sequence 6896, Ap
44	28	93.3	676	24	US-60-258-275-375	Sequence 375, App
45	28	93.3	703	16	US-09-252-991A-18391	Sequence 18391, A

ALIGNMENTS

RESULT 1
US-09-464-908-1
; Sequence 1, Application US/09464908
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; TITLE OF INVENTION: Selective inhibitors of MMP-12
; FILE REFERENCE: HMR2026A
; CURRENT APPLICATION NUMBER: US/09/464,908
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/155,223
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic construct
; US-09-464-908-1

Query Match 100.0%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 1 PLGLAR 6

RESULT 2
US-09-588-417-6
; Sequence 6, Application US/09588417

GENERAL INFORMATION:
APPLICANT: Fourie, Anne
APPLICANT: Karlsson, Lars
APPLICANT: Thurmond, Rob
TITLE OF INVENTION: Metalloprotease Peptide Substrates And Methods
FILE REFERENCE: ORT-1220
CURRENT APPLICATION NUMBER: US/09/588,417
CURRENT FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-09-588-417-6

Query Match 100.0%; Score 30; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||
Db 2 PLGLAR 7

RESULT 3
US-09-902-540-12523
Sequence 12523, Application US/09902540
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 12523
LENGTH: 128
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-12523

Query Match 100.0%; Score 30; DB 23; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||
Db 77 PLGLAR 82

RESULT 4
US-09-758-472-5376
Sequence 5376, Application US/09758472
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PH001
CURRENT APPLICATION NUMBER: US/09/758,472
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9632
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5376
LENGTH: 177
TYPE: PRT
ORGANISM: Homo sapiens
US-09-758-472-5376

Query Match 100.0%; Score 30; DB 21; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||
Db 53 PLGLAR 58

RESULT 5
US-09-252-991A-19176
Sequence 19176, Application US/09252991A
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19176
LENGTH: 203
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19176

Query Match 100.0%; Score 30; DB 16; Length 203;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||
Db 130 PLGLAR 135

RESULT 6
US-09-252-691-6030
Sequence 6030, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 6030
LENGTH: 230
TYPE: PRT
ORGANISM: Enterobacter cloacae
US-09-252-691-6030

Query Match 100.0%; Score 30; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
|||||

Db 96 PLGLAR 101

RESULT 7

US-09-252-691C-6030
; Sequence 6030, Application US/09252691C
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
; TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.135
; CURRENT APPLICATION NUMBER: US/09/252.691C
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/094.145
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: US 60/074.787
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 11326
; SEQ ID NO 6030
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-09-252-691C-6030

Query Match 100.0%; Score 30; DB 16; Length 230;

Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 96 PLGLAR 101

RESULT 8

PCT-US01-14827-12965
; Sequence 12965, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577.408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 12965
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-14827-12965

Query Match 100.0%; Score 30; DB 1; Length 277;

Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 153 PLGLAR 158

RESULT 9

US-09-252-991A-19047
; Sequence 19047, Application US/09252991A
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074.788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094.190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19047
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19047

Query Match 100.0%; Score 30; DB 16; Length 293;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 89 PLGLAR 94

RESULT 10

US-09-562-737-6
; Sequence 6, Application US/09562737
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562.737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-6

Query Match 100.0%; Score 30; DB 19; Length 333;

Best Local Similarity 100.0%; Pred. No. 6.4e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 2 PLGLAR 7

RESULT 11

PCT-US01-16450-2736
; Sequence 2736, Application PC/TUS0116450
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/205.515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450-2736

Query Match 100.0%; Score 30; DB 1; Length 362;

Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 87 PLGLAR 92

RESULT 12

PCT-US01-16450A-2736
; Sequence 2736, Application PC/TUS0116450A
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA131PCT
; CURRENT APPLICATION NUMBER: PCT/US01/16450A
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2820
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2736
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-16450A-2736

Query Match 100.0%; Score 30; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 87 PLGLAR 92

RESULT 13

US-09-731-872-280
; Sequence 280, Application US/09731872
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US3 REG
; CURRENT APPLICATION NUMBER: US/09/731,872
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 280
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-09-731-872-280

Query Match 100.0%; Score 30; DB 21; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 87 PLGLAR 92

RESULT 14

US-09-876-997-280
; Sequence 280, Application US/09876997
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean Baptiste
; APPLICANT: Bouqueleret, Lydie
; APPLICANT: Jobert, Severin
; TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
; FILE REFERENCE: 78 US4 CIP
; CURRENT APPLICATION NUMBER: US/09/876,997
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/731,872
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/187,470
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 60/169,629
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 482
; SOFTWARE: Patent.pm
; SEQ ID NO 280
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-09-876-997-280

Query Match 100.0%; Score 30; DB 22; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 87 PLGLAR 92

RESULT 15

US-60-169-629-495
; Sequence 495, Application US/60169629
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bouqueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: CDNAS for Secreted Proteins
; FILE REFERENCE: GENSET.071PRF
; CURRENT APPLICATION NUMBER: US/60/169,629
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 715
; SOFTWARE: Patent.pm
; SEQ ID NO 495
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -40...-1
US-60-169-629-495

Query Match 100.0%; Score 30; DB 24; Length 362;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 87 PLGLAR 92

Search completed: February 28, 2002, 16:49:23
Job time: 198 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28; 2002, 16:46:05 ; Search time 14.33 Seconds
(without alignments)
23.705 Million cell updates

Title: 09-876091
Perfect score: 30
Sequence: 1 plqlar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 258822 seqs, 56616433 residues

Total number of hits satisfying chosen parameters: 258822

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database : Pending_Patents_AA_New.*
1: /cgn2_6/pdodata/2/paa/pct_NEW_COMB pep.*
2: /cgn2_6/pdodata/2/paa/US05_NEW_COMB pep.*
3: /cgn2_6/pdodata/2/paa/US07_NEW_COMB pep.*
4: /cgn2_6/pdodata/2/paa/US08_NEW_COMB pep.*
5: /cgn2_6/pdodata/2/paa/US09_NEW_COMB pep.*
6: /cgn2_6/pdodata/2/paa/US10_NEW_COMB pep.*
7: /cgn2_6/pdodata/2/paa/US10_NEW_COMB pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

CONFIDENTIAL

Result No.	Score	Query Match	Length	DB	ID	Description
1	30	100.0	8	6	US-10-050-200-39	Sequence 39, Appl
2	30	100.0	119	5	US-09-708-427-74176	Sequence 74176, A
3	30	100.0	219	6	US-10-013-127-10477	Sequence 10477, A
4	30	100.0	489	5	US-09-989-723-138	Sequence 138, App
5	30	100.0	489	5	US-09-989-724-138	Sequence 138, App
6	30	100.0	489	5	US-09-989-730-138	Sequence 138, App
7	30	100.0	489	5	US-09-990-436-138	Sequence 138, App
8	30	100.0	489	5	US-09-990-444-138	Sequence 138, App
9	30	100.0	489	5	US-09-989-721-138	Sequence 138, App
10	30	100.0	489	5	US-09-989-722-138	Sequence 138, App
11	30	100.0	489	5	US-09-989-725-138	Sequence 138, App
12	30	100.0	489	5	US-09-989-726-138	Sequence 138, App
13	30	100.0	489	5	US-09-989-727-138	Sequence 138, App
14	30	100.0	489	5	US-09-989-728-138	Sequence 138, App
15	30	100.0	489	5	US-09-989-731-138	Sequence 138, App
16	30	100.0	489	5	US-09-989-732-138	Sequence 138, App
17	30	100.0	489	5	US-09-989-734-138	Sequence 138, App
18	30	100.0	489	5	US-09-990-437-138	Sequence 138, App
19	30	100.0	489	5	US-09-990-438-138	Sequence 138, App
20	30	100.0	489	5	US-09-990-440-138	Sequence 138, App
21	30	100.0	489	5	US-09-990-441-138	Sequence 138, App
22	30	100.0	489	5	US-09-989-279-138	Sequence 138, App
23	30	100.0	489	5	US-09-989-735-138	Sequence 138, App
24	30	100.0	489	5	US-09-990-439-138	Sequence 138, App
25	30	100.0	489	5	US-09-990-562-138	Sequence 138, App
26	30	100.0	489	5	US-09-997-349-138	Sequence 138, App

ALIGNMENTS

RESULT

```

US-10-050-200-39
: Sequence 39, Application US/10050200
:
: GENERAL INFORMATION:
: APPLICANT: Fourie, Anne
: APPLICANT: Cotes, Fawn
: APPLICANT: Karlsson, Lars
: TITLE OF INVENTION: Aggrucanase-1 a
: FILE REFERENCE: ORT-1417
: CURRENT APPLICATION NUMBER: US/10/0
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 39
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: peptide substra
US-10-050-200-39

```

Query Match	100.0%	Score 30;	DB 6;	Length 8;
Best Local Similarity	100.0%;	pred. No. 2.3e+05;		
Matches	6;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

Qy	1	plglar	6
Db	3	PLGLAR	8

RESULT

```

US-09-708-427-74176
; Sequence 74176, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED D
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74176
; LENGTH: 119
; TYPE: PR1
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature

```

; LOCATION: 1..119
; OTHER INFORMATION: xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: 1..119
; OTHER INFORMATION: Ceres Seq. ID 1945018
US-09-708-427-74176

Query Match 100.0%; Score 30; DB 5; Length 119;

Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0

Qy 1 plglar 6
| | | | |
Db 66 PLGLAR 71

RESULT 3

US-10-015-127-10477
; Sequence 10477, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Spingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 10477
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Spingomonas elodea
US-10-013-127-10477

Query Match 100.0%; Score 30; DB 6; Length 219;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |
Db 63 PLGLAR 68

RESULT 4

US-09-989-723-138
; Sequence 138, Application US/09989723
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10

;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690

;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 plglar 6
|||||
Db 214 PLGLAR 219

RESULT 5

US-09-989-724-138
; Sequence 138, Application US/09989724
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC67
; CURRENT APPLICATION NUMBER: US/09/989, 724
; CURRENT FILING DATE: 2001-11-20

1 PRIOR APPLICATION NUMBER: 60/049787
2 PRIOR FILING DATE: 1997-06-16
3 PRIOR APPLICATION NUMBER: 60/062250
4 PRIOR FILING DATE: 1997-10-17
5 PRIOR APPLICATION NUMBER: 60/065186
6 PRIOR FILING DATE: 1997-11-12
7 PRIOR APPLICATION NUMBER: 60/065311
8 PRIOR FILING DATE: 1997-11-13
9 PRIOR APPLICATION NUMBER: 60/066770
10 PRIOR FILING DATE: 1997-11-24
11 PRIOR APPLICATION NUMBER: 60/075945
12 PRIOR FILING DATE: 1998-02-25
13 PRIOR APPLICATION NUMBER: 60/078910
14 PRIOR FILING DATE: 1998-03-20
15 PRIOR APPLICATION NUMBER: 60/083322
16 PRIOR FILING DATE: 1998-04-28
17 PRIOR APPLICATION NUMBER: 60/084600
18 PRIOR FILING DATE: 1998-05-07
19 PRIOR APPLICATION NUMBER: 60/087106
20 PRIOR FILING DATE: 1998-05-28
21 PRIOR APPLICATION NUMBER: 60/087607
22 PRIOR FILING DATE: 1998-06-02
23 PRIOR APPLICATION NUMBER: 60/087609
24 PRIOR FILING DATE: 1998-06-02
25 PRIOR APPLICATION NUMBER: 60/087759
26 PRIOR FILING DATE: 1998-06-02
27 PRIOR APPLICATION NUMBER: 60/087827
28 PRIOR FILING DATE: 1998-06-03
29 PRIOR APPLICATION NUMBER: 60/088021
30 PRIOR FILING DATE: 1998-06-04
31 PRIOR APPLICATION NUMBER: 60/088025
32 PRIOR FILING DATE: 1998-06-04
33 PRIOR APPLICATION NUMBER: 60/088026
34 PRIOR FILING DATE: 1998-06-04
35 PRIOR APPLICATION NUMBER: 60/088028
36 PRIOR FILING DATE: 1998-06-04
37 PRIOR APPLICATION NUMBER: 60/088029
38 PRIOR FILING DATE: 1998-06-04
39 PRIOR APPLICATION NUMBER: 60/088030
40 PRIOR FILING DATE: 1998-06-04
41 PRIOR APPLICATION NUMBER: 60/088033
42 PRIOR FILING DATE: 1998-06-04
43 PRIOR APPLICATION NUMBER: 60/088326
44 PRIOR FILING DATE: 1998-06-04
45 PRIOR APPLICATION NUMBER: 60/088167
46 PRIOR FILING DATE: 1998-06-05
47 PRIOR APPLICATION NUMBER: 60/088202
48 PRIOR FILING DATE: 1998-06-05
49 PRIOR APPLICATION NUMBER: 60/088212
50 PRIOR FILING DATE: 1998-06-05
51 PRIOR APPLICATION NUMBER: 60/088217
52 PRIOR FILING DATE: 1998-06-05
53 PRIOR APPLICATION NUMBER: 60/088655
54 PRIOR FILING DATE: 1998-06-09
55 PRIOR APPLICATION NUMBER: 60/088734
56 PRIOR FILING DATE: 1998-06-10
57 PRIOR APPLICATION NUMBER: 60/088738
58 PRIOR FILING DATE: 1998-06-10
59 PRIOR APPLICATION NUMBER: 60/088742
60 PRIOR FILING DATE: 1998-06-10
61 PRIOR APPLICATION NUMBER: 60/088810
62 PRIOR FILING DATE: 1998-06-10
63 PRIOR APPLICATION NUMBER: 60/088824
64 PRIOR FILING DATE: 1998-06-10
65 PRIOR APPLICATION NUMBER: 60/088826
66 PRIOR FILING DATE: 1998-06-10
67 PRIOR APPLICATION NUMBER: 60/088858
68 PRIOR FILING DATE: 1998-06-11
69 PRIOR APPLICATION NUMBER: 60/088861
70 PRIOR FILING DATE: 1998-06-11
71 PRIOR APPLICATION NUMBER: 60/088876
72 PRIOR FILING DATE: 1998-06-11
73 PRIOR APPLICATION NUMBER: 60/089105

74 PRIOR FILING DATE: 1998-06-12
75 PRIOR APPLICATION NUMBER: 60/089440
76 PRIOR FILING DATE: 1998-06-16
77 PRIOR APPLICATION NUMBER: 60/089512
78 PRIOR FILING DATE: 1998-06-16
79 PRIOR APPLICATION NUMBER: 60/089514
80 PRIOR FILING DATE: 1998-06-16
81 PRIOR APPLICATION NUMBER: 60/089532
82 PRIOR FILING DATE: 1998-06-17
83 PRIOR APPLICATION NUMBER: 60/089538
84 PRIOR FILING DATE: 1998-06-17
85 PRIOR APPLICATION NUMBER: 60/089598
86 PRIOR FILING DATE: 1998-06-17
87 PRIOR APPLICATION NUMBER: 60/089599
88 PRIOR FILING DATE: 1998-06-17
89 PRIOR APPLICATION NUMBER: 60/089600
90 PRIOR FILING DATE: 1998-06-17
91 PRIOR APPLICATION NUMBER: 60/089653
92 PRIOR FILING DATE: 1998-06-17
93 PRIOR APPLICATION NUMBER: 60/089801
94 PRIOR FILING DATE: 1998-06-18
95 PRIOR APPLICATION NUMBER: 60/089907
96 PRIOR FILING DATE: 1998-06-18
97 PRIOR APPLICATION NUMBER: 60/089908
98 PRIOR FILING DATE: 1998-06-18
99 PRIOR APPLICATION NUMBER: 60/089947
100 PRIOR FILING DATE: 1998-06-19
101 PRIOR APPLICATION NUMBER: 60/089948
102 PRIOR FILING DATE: 1998-06-19
103 PRIOR APPLICATION NUMBER: 60/089952
104 PRIOR FILING DATE: 1998-06-19
105 PRIOR APPLICATION NUMBER: 60/090246
106 PRIOR FILING DATE: 1998-06-22
107 PRIOR APPLICATION NUMBER: 60/090252
108 PRIOR FILING DATE: 1998-06-22
109 PRIOR APPLICATION NUMBER: 60/090254
110 PRIOR FILING DATE: 1998-06-22
111 PRIOR APPLICATION NUMBER: 60/090349
112 PRIOR FILING DATE: 1998-06-23
113 PRIOR APPLICATION NUMBER: 60/090355
114 PRIOR FILING DATE: 1998-06-23
115 PRIOR APPLICATION NUMBER: 60/090429
116 PRIOR FILING DATE: 1998-06-24
117 PRIOR APPLICATION NUMBER: 60/090431
118 PRIOR FILING DATE: 1998-06-24
119 PRIOR APPLICATION NUMBER: 60/090435
120 PRIOR FILING DATE: 1998-06-24
121 PRIOR APPLICATION NUMBER: 60/090444
122 PRIOR FILING DATE: 1998-06-24
123 PRIOR APPLICATION NUMBER: 60/090535
124 PRIOR FILING DATE: 1998-06-24
125 PRIOR APPLICATION NUMBER: 60/090540
126 PRIOR FILING DATE: 1998-06-24
127 PRIOR APPLICATION NUMBER: 60/090542
128 PRIOR FILING DATE: 1998-06-24
129 PRIOR APPLICATION NUMBER: 60/090557
130 PRIOR FILING DATE: 1998-06-24
131 PRIOR APPLICATION NUMBER: 60/090676
132 PRIOR FILING DATE: 1998-06-25
133 PRIOR APPLICATION NUMBER: 60/090678
134 PRIOR FILING DATE: 1998-06-25
135 PRIOR APPLICATION NUMBER: 60/090690
136 PRIOR FILING DATE: 1998-06-25
137 PRIOR APPLICATION NUMBER: 60/090694
138 PRIOR FILING DATE: 1998-06-25
139 PRIOR APPLICATION NUMBER: 60/090695
140 PRIOR FILING DATE: 1998-06-25
141 PRIOR APPLICATION NUMBER: 60/090696
142 PRIOR FILING DATE: 1998-06-25

```

; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

```

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 214 PLGLAR 219

RESULT 6

US-09-989-730-138

; Sequence 138, Application US/09989730

; GENERAL INFORMATION:

```

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavins, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311

```

```

; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16

```

;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090576
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478

;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plqlar 6
Db 214 PLGLAR 219

RESULT 7

US-09-990-436-138
; Sequence 138, Application US/09990436
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 214 PLGLAR 219
|||||

RESULT 8

US-09-990-444-138
; Sequence 138. Application US/09990444

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC19

; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18

; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182

; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 214 PLGLAR 219
|||||

RESULT 9
US-09-989-721-138
; Sequence 138, Application US/09989721
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989, 721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels

Oy 1 plglar 6
Db 214 PLGLAR 219

RESULT 10

US-09-989-722-138
; Sequence 138, Application US/09989722
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989, 722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028

; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22

;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 214 PLGLAR 219
| | | | |

RESULT 1+
US-09-989-725-138

;; Sequence 138, Application US/09989725
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730P1C71
;; CURRENT APPLICATION NUMBER: US/09/989,725
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04

; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429

; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
| | | | |

Db 214 PLGLAR 219

RESULT 12

US-09-989-726-138
; Sequence 138, Application US/09989726
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24

;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6

Db 214 PLGLAR 219

RESULT 13

US-09-989-727-138

; Sequence 138, Application US/09989727

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hauspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PLC65
; CURRENT APPLICATION NUMBER: US/09/989,727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10

;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088876
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089440
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089532
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089599
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089600
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089907
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089908
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/089947
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089948
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/089952
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: 60/090246
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090252
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090254
;; PRIOR FILING DATE: 1998-06-22
;; PRIOR APPLICATION NUMBER: 60/090349
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090355
;; PRIOR FILING DATE: 1998-06-23
;; PRIOR APPLICATION NUMBER: 60/090429
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090431
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090535
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plqlar 6

Db 214 plqlar 219

RESULT 14

US-09-989-728-138

; Sequence 138, Application US/09989728

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerlitsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT APPLICATION NUMBER: US/09/989,728
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824

PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25

;; PRIOR APPLICATION NUMBER: 60/090678
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0;

Qy 1 p1glar 6

Db 214 PLGLAR 219

RESULT 15

US-09-989-731-138
Sequence 138, Application US/09989731

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

;; FILE REFERENCE: P2730PIC70
;; CURRENT APPLICATION NUMBER: US/09/989,731
;; PRIOR FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066770
;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/083322
;; PRIOR FILING DATE: 1998-04-28
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
;; PRIOR FILING DATE: 1998-05-28
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087609
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087759
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/087827
;; PRIOR FILING DATE: 1998-06-03
;; PRIOR APPLICATION NUMBER: 60/088021
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088025
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088026
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088028
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088029
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088030
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088033
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088326
;; PRIOR FILING DATE: 1998-06-04
;; PRIOR APPLICATION NUMBER: 60/088167
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088202
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088212
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088217
;; PRIOR FILING DATE: 1998-06-05
;; PRIOR APPLICATION NUMBER: 60/088655
;; PRIOR FILING DATE: 1998-06-09
;; PRIOR APPLICATION NUMBER: 60/088734
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088738
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088742
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088810
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088824
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088826
;; PRIOR FILING DATE: 1998-06-10
;; PRIOR APPLICATION NUMBER: 60/088858
;; PRIOR FILING DATE: 1998-06-11
;; PRIOR APPLICATION NUMBER: 60/088861
;; PRIOR FILING DATE: 1998-06-11

;
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089440
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089948
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090246
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090252
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090254
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090355
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090435
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090444
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090540
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090542
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090676
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090678
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090690
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090694
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695

;
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090696
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472

Query Match 100.0%; Score 30; DB 5; Length 489;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

|||||

Db 214 PLGLAR 219

Search completed: February 28, 2002, 16:49:44
Job time: 219 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:46:05 ; Search time 12.48 seconds
(without alignments)
10.819 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	77	4	US-09-246-500B-2
2	28	93.3	422	2	US-08-403-852D-17
3	28	93.3	422	3	US-08-510-646B-18
4	28	93.3	422	4	US-09-231-818-17
5	27	90.0	275	4	US-08-976-255-16
6	27	90.0	472	4	US-08-976-255-17
7	26	86.7	568	1	US-08-262-424-7
8	26	86.7	568	2	US-08-493-197-7
9	26	86.7	568	2	US-08-717-587A-4
10	26	86.7	568	3	US-08-883-610A-4
11	26	86.7	568	4	US-08-936-094A-4
12	26	86.7	568	5	PCT-US95-07844-7
13	25	83.3	15	2	US-08-368-834-14
14	25	83.3	15	2	US-08-447-154-14
15	25	83.3	16	3	US-09-136-251-6
16	25	83.3	70	4	US-08-965-056-93
17	25	83.3	84	4	US-08-905-223-404
18	25	83.3	104	4	US-08-965-056-91
19	25	83.3	114	2	US-08-473-020A-21
20	25	83.3	114	2	US-08-473-020A-22
21	25	83.3	114	2	US-08-473-020A-23
22	25	83.3	114	2	US-08-473-020A-26
23	25	83.3	114	2	US-08-473-020A-27
24	25	83.3	120	2	US-08-997-080-80
25	25	83.3	120	2	US-08-997-362-80
26	25	83.3	120	3	US-08-873-970-80
27	25	83.3	120	4	US-09-095-855-80

28 83.3 122 2 US-08-473-020A-25
29 25 83.3 198 4 US-08-965-056-90
30 25 83.3 215 2 US-08-997-080-117
31 25 83.3 215 2 US-08-997-362-117
32 25 83.3 215 4 US-09-095-855-117
33 25 83.3 240 4 US-08-913-014A-1
34 25 83.3 267 1 US-08-570-929-2
35 25 83.3 269 3 US-08-759-463-2
36 25 83.3 269 4 US-09-328-153-2
37 25 83.3 286 4 US-09-188-930-137
38 25 83.3 299 4 US-08-944-483-66
39 25 83.3 301 1 US-08-420-235B-47
40 25 83.3 301 2 US-08-343-101A-22
41 25 83.3 301 3 US-09-183-688-22
42 25 83.3 301 3 US-08-793-624-47
43 25 83.3 355 4 US-09-194-905-10
44 25 83.3 389 2 US-08-485-449-6
45 25 83.3 422 4 US-09-151-102-2

ALIGNMENTS

RESULT 1

US-09-246-500B-2
; Sequence 2, Application US/09246500B
; Patent No. 6235494
; GENERAL INFORMATION:
; APPLICANT: Hugli, Tony E.
; TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
; TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods
; FILE REFERENCE: 24730-2204
; CURRENT APPLICATION NUMBER: US/09/246,500B
; CURRENT FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Pig C3a Anaphylatoxin
US-09-246-500B-2

Query Match 100.0%; Score 30; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 72 PLGLAR 77

RESULT 2

US-08-403-852D-17
; Sequence 17, Application US/08403852D
; Patent No. 5891695
; GENERAL INFORMATION:
; APPLICANT: Blanc, Veronique
; APPLICANT: Blanche, Francis
; APPLICANT: Crouzet, Joel
; APPLICANT: Jacques, Nathalie
; APPLICANT: Lacroix, Patricia
; APPLICANT: Thibaut, Denis
; APPLICANT: zagorec, Monique
; APPLICANT: Debussche, Laurent
; APPLICANT: De Crecy-Lagard, Valerie
; TITLE OF INVENTION: Polypeptides Involved In The
; TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: US/08/403,852D
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION DATA:
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: FR 92/11441
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-403-852D-17

Query Match 93.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgar 6
Db 188 PLGIAR 193

RESULT 3
US-08-510-646B-18
Sequence 18, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION DATA:
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: FR 92/11441
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-510-646B-18

Query Match 93.3%; Score 28; DB 3; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgar 6
Db 188 PLGIAR 193

RESULT 4
US-09-231-818-17
Sequence 17, Application US/09231818
Patent No. 6171846
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanc, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/231,818
FILING DATE:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,852
FILING DATE: 10-MAY-1995
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-231-818-17

Query Match 93.3%; Score 28; DB 4; Length 422;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 188 PLGIAR 193

RESULT 5
US-08-976-255-16
Sequence 16, Application US/08976255
Patent No. 6136581
GENERAL INFORMATION:
APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-976-255-16

Query Match 90.0%; Score 27; DB 4; Length 275;
Best Local Similarity 83.3%; Pred. No. 78;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 60 PLGLSR 65

RESULT 6
US-08-976-255-17
Sequence 17, Application US/08976255
Patent No. 6136581
GENERAL INFORMATION:
APPLICANT: Jono, Keith E.
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: KINASE GENES AND USES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,255
FILING DATE: No. 6136581ember 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031,675
FILING DATE: No. 6136581ember 22, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 229/182
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-976-255-17

Query Match 90.0%; Score 27; DB 4; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 125 PLGLSR 130

```
RESULT 7
US-08-262-424-7
; Sequence 7, Application US/08262424
; Patent No. 5604111
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalate
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-262-424-7

Query Match 86.7%; Score 26; DB 1; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 146 PIGIAR 151

RESULT 8
US-08-493-197-7
; Sequence 7, Application US/08493197
; Patent No. 5837833
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalate
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/493,197
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-493-197-7

Query Match 86.7%; Score 26; DB 2; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
Db 146 PIGIAR 151

RESULT 9
US-08-717-587A-4
; Sequence 4, Application US/08717587A
; Patent No. 5912125
; GENERAL INFORMATION:
; APPLICANT: Peck, Ammon B.
; TITLE OF INVENTION: Materials and Methods for Detection of
; TITLE OF INVENTION: Oxalobacter
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,587A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/493,197
; FILING DATE: 20-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/262,424
; FILING DATE: 20-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Doran R.
; REGISTRATION NUMBER: 38,261
; REFERENCE/DOCKET NUMBER: UF-145C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352-375-8100
; TELEFAX: 352-372-5800
```

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-717-587A-4

Query Match 86.7%; Score 26; DB 2; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
11111
DB 146 PIGIAR 151

RESULT 10

US-08-883-610A-4
Sequence 4, Application US/08883610A
Patent No. 6090628

GENERAL INFORMATION:
APPLICANT: Peck, Ammon B.
APPLICANT: Sidhu, Harmeet
TITLE OF INVENTION: Materials and Methods for Detection of
TITLE OF INVENTION: Oxalobacter
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,610A
FILING DATE: 26-JUN-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/717,587
FILING DATE: 27-SEP-1996

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/493,197
FILING DATE: 20-JUN-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/262,424
FILING DATE: 20-JUN-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: UF-145C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-610A-4

Query Match 86.7%; Score 26; DB 3; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
11111
DB 146 PIGIAR 151

RESULT 11

US-08-936-094A-4
Sequence 4, Application US/08936094A
Patent No. 6214980

GENERAL INFORMATION:
APPLICANT: Peck, Ammon B.
APPLICANT: Sidhu, Harmeet
TITLE OF INVENTION: Materials and Methods for Detection of Oxalobacter formigenes
FILE REFERENCE: UF-145C4
CURRENT APPLICATION NUMBER: US/08/936,094A
CURRENT FILING DATE: 1997-09-23
PRIOR APPLICATION NUMBER: 08/883,610
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: 08/717,587
PRIOR FILING DATE: 1996-09-27
PRIOR APPLICATION NUMBER: 08/493,197
PRIOR FILING DATE: 1995-06-20
PRIOR APPLICATION NUMBER: 08/262,424
PRIOR FILING DATE: 1994-06-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 568
TYPE: PRT
ORGANISM: Oxalobacter formigenes
US-08-936-094A-4

Query Match 86.7%; Score 26; DB 4; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglar 6
11111
DB 146 PIGIAR 151

RESULT 12

PCT-US95-07844-7
Sequence 7, Application PC/TUS9507844
GENERAL INFORMATION:

APPLICANT:
APPLICANT: Street address: 223 Grinter Hall
APPLICANT: City: Gainesville
APPLICANT: State/Province: Florida
APPLICANT: Country: US
APPLICANT: Postal code/zip: 32611
APPLICANT: Phone number: 904-392-8929
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for Detection of
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

US-08-936-094A-4

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07844
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/262,424
FILING DATE: 20-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-07844-7

Query Match 86.7%; Score 26; DB 5; Length 568;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 146 PIGIAR 151

RESULT 13
US-08-368-834-14
Sequence 14, Application US/08368834
Patent No. 5874405
GENERAL INFORMATION:
APPLICANT: Birnbaum, Gary
APPLICANT: Kotilinek, Linda K.
TITLE OF INVENTION: Heat Shock Protein Peptides That Share
TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase and
TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous System
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5874405west Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,834
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 600.3030501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-9081
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-834-14

Query Match 83.3%; Score 25; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plglar 6
Db 2 PLGLKR 7

RESULT 14
US-08-447-154-14
Sequence 14, Application US/08447154
Patent No. 5958416
GENERAL INFORMATION:
APPLICANT: Birnbaum, Gary
APPLICANT: Kotilinek, Linda K.
TITLE OF INVENTION: Heat Shock Protein Peptides That
TITLE OF INVENTION: Share
TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase
TITLE OF INVENTION: and
TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous
TITLE OF INVENTION: System
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5958416west Center
CITY: Minneapolis
STATE: Minnesota
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,154
FILING DATE: 23-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/368,834
FILING DATE: 16-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Katherine M.
REGISTRATION NUMBER: 36,848
REFERENCE/DOCKET NUMBER: 600.3090501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-154-14

Query Match 83.3%; Score 25; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglar 6
| | | | |
Db 2 PLGLKR 7

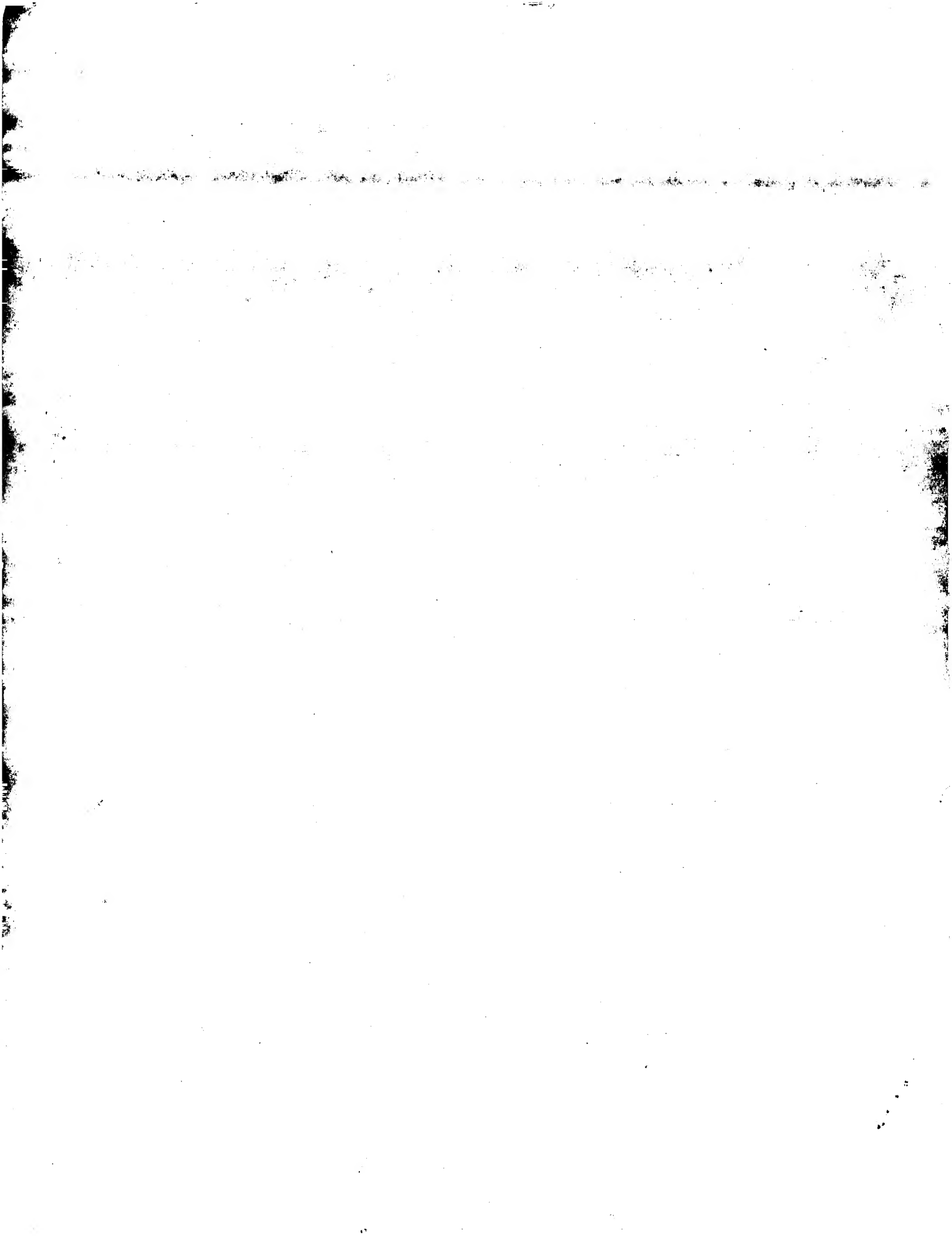
RESULT 15

US-09-136-251-6
; Sequence 6, Application US/09136251A
; Patent No. 6127156
; GENERAL INFORMATION:
; APPLICANT: HOSHINO, Tatsuo
; APPLICANT: MIYAZAKI, Taro
; APPLICANT: OJIMA, Setsuko
; APPLICANT: SHINJOH, Masako
; APPLICANT: TOMIYAMA, No. 6127156ibumi
; TITLE OF INVENTION: D-SORBITOL DEHYDROGENASE GENE
; FILE REFERENCE: D-Sorbitol Dehydrogenase Gene
; CURRENT APPLICATION NUMBER: US/09/136,251A
; CURRENT FILING DATE: 1998-08-19
; EARLIER APPLICATION NUMBER: EP 97114432.4
; EARLIER FILING DATE: 1997-08-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Gluconobacter suboxydans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (13)
US-09-136-251-6

Query Match 83.3%; Score 25; DB 3; Length 16;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglar 6
| | | | |
Db 7 PLGTAR 12

Search completed: February 28, 2002, 16:47:42
Job time: 97 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:49:45 ; Search time 12.68 seconds
(without alignments)
36.045 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 315

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	17	56.7	4	2 A32039	tyrosine-melanocyt
2	13	43.3	5	2 A44955	alkanal monooxygen
3	11	36.7	4	2 I61883	protamine pl - ora
4	11	36.7	4	2 I37013	protamine pl - Cer
5	11	36.7	4	2 I84439	protamine pl - sav
6	11	36.7	5	2 I39966	ribosomal protein
7	11	36.7	5	2 I39966	ribosomal protein
8	11	36.7	5	2 I39965	ribosomal protein
9	11	36.7	5	2 G44817	27.5 kda structura
10	11	36.7	5	2 I44817	27.5K structural p
11	11	36.7	5	2 E44817	27.5K structural p
12	11	36.7	5	2 C44817	28.5K structural p
13	11	36.7	5	2 A44817	28K structural pro
14	11	36.7	6	2 I37027	protamine pl - gor
15	11	36.7	6	2 PT0568	T-cell receptor be
16	10	33.3	4	2 S18401	thyroglobulin - do
17	10	33.3	4	2 I38888	CoI intron 16 prot
18	10	33.3	4	2 A32480	achatin-I - giant
19	10	33.3	4	2 PT0240	Ig heavy chain CRD
20	10	33.3	4	2 A53284	T-cell receptor be
21	10	33.3	4	2 PT0721	T-cell receptor be
22	10	33.3	5	2 D48823	synaptosomal-assoc
23	10	33.3	5	2 PT0713	T-cell receptor be
24	10	33.3	6	2 S11024	hydrogensulfite re
25	10	33.3	6	2 B56979	collagen alpha 1(I
26	10	33.3	6	2 H48394	glycoprotein compo
27	10	33.3	6	2 A20186	fatty-acid synthas
28	10	33.3	6	2 PT0643	T-cell receptor be
29	10	33.3	6	2 PT0621	T-cell receptor be

30	10	33.3	6	2 PT0560	T-cell receptor be
31	10	33.3	6	2 PT0718	T-cell receptor be
32	10	33.3	6	2 PT0589	T-cell receptor be
33	10	33.3	6	2 PT0727	T-cell receptor be
34	10	33.3	6	2 PT0730	T-cell receptor be
35	9	30.0	3	2 PQ0010	angiotensin-conver
36	9	30.0	5	2 E60274	major protein anti
37	9	30.0	5	2 S51077	alpha-amylase - ri
38	9	30.0	5	2 B37988	acid proteinase li
39	9	30.0	5	2 S62883	seminal plasma pro
40	9	30.0	6	2 A35890	RNA-directed DNA p
41	9	30.0	6	2 A61049	halo-toxin - Pseud
42	9	30.0	6	2 PQ0008	angiotensin-conver
43	9	30.0	6	2 A27696	contraction-inhibi
44	9	30.0	6	2 B27696	contraction-inhibi
45	8	26.7	3	2 B23751	spinal cord peptid

ALIGNMENTS

RESULT 1

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C;Accession: A32039

R;Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact
A;Reference number: A32039; MUID:89123285

A;Accession: A32039

A;Molecule type: protein

A;Residues: 1-4 <HOR>

A;Experimental source: brain

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end

F;4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 56.7%; Score 17; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.2e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3

Db 2 PLG 4

RESULT 2

A44955

alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragm
C;Species: Vibrio harveyi

C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000

C;Accession: A44955

R;Paquette, O.; Tu, S.C.

Photochem. Photobiol. 50, 817-825, 1989

A;Title: Chemical modification and characterization of the alpha cysteine 106 at the

A;Reference number: A44955; MUID:90175700

A;Accession: A44955

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-5 <PAQ>

C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match

Best Local Similarity 43.3%; Score 13; DB 2; Length 5;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 glar 6

Db 2 GIXR 5

```

RESULT 3
I61883
protamine P1 - orangutan (fragment)
C:Species: Pongo pygmaeus (orangutan)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I61883
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I61883
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:212146; NID:g38156; PIDN:CAA78130.1; PID:g4379372

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 4
I37013
protamine P1 - Cercopithecus patas (fragment)
C:Species: Cercopithecus patas
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I37013
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I37013
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:212150; NID:g22814; PIDN:CAA78134.1; PID:g4377415

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 5
I84439
protamine P1 - savannah baboon (fragment)
C:Species: Papio hamadryas doquiera (savannah baboon)
C>Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 21-Jul-2000
C:Accession: I84439
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I84439
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:212147; NID:g38134; PIDN:CAA78131.1; PID:g4379349

Query Match 36.7%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 6
I39964
ribosomal protein S4 - Bacillus circulans (fragment)
C:Species: Bacillus circulans
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39964
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39964
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99041; NID:g143471
C:Genetics:
A:Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 7
I39966
ribosomal protein S4 - Bacillus licheniformis (fragment)
C:Species: Bacillus licheniformis
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39966
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
A:Accession: I39966
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: GB:M99043; NID:g143475
C:Genetics:
A:Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:|
Db 1 MAR 3

RESULT 8
I39965
ribosomal protein S4 - Bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C>Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 19-Jul-1996
C:Accession: I39965
R:Grundy, F.J.; Henkin, T.M.
J. Bacteriol. 174, 6763-6770, 1992
A:Title: Characterization of the Bacillus subtilis rpsD regulatory target site.
A:Reference number: I39963; MUID:93015735
```


A;Accession: I39965
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-5 <RES>
A;Cross-references: GB:M99042; NID:g143473
C;Genetics:
A;Gene: rpsD

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lgl 6
:||
Db 1 MAR 3

RESULT 9

G44817
27.5K structural protein - Leuconostoc oenos phase P32 (fragment)
C;Species: Leuconostoc oenos phase P32
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: G44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: G44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 10

I44817
27.5K structural protein - Leuconostoc oenos phase P37 (fragment)
C;Species: Leuconostoc oenos phase P37
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: I44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: I44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 11

E44817
27.5K structural protein - Leuconostoc oenos phase P54 (fragment)
C;Species: Leuconostoc oenos phase P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998

C;Accession: E44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: E44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 12

C44817
28.5K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)
C;Species: Leuconostoc oenos phase PAT5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: C44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: C44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 13

A44817
28K structural protein - Leuconostoc oenos phase PZtl1-15 (fragment)
C;Species: Leuconostoc oenos phase PZtl1-15
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: A44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: A44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 36.7%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lgl 4
:||
Db 3 VGL 5

RESULT 14

I37027
protamine P1 - gorilla (fragment)

C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jul-2000
C:Accession: I37027
R:Queralt, R.; Oliva, R.
Gene 133, 197-204, 1993
A:Title: Identification of conserved potential regulatory sequences of the protamine-end
A:Reference number: I37013; MUID:94040810
A:Accession: I37027
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:Cross-references: EMBL:Z12145; NID:g22910; PIDN:CAA78129.1; PID:g579612

Query Match 36.7%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
:||
Db 1 MAR 3

RESULT 15

PT0568
T-cell receptor beta chain V-D-J region (141-1C) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0568
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0568
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 36.7%; Score 11; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.2e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 glar 6
:|||
Db 3 GDAR 6

Search completed: February 28, 2002, 16:51:38
Job time: 113 sec

OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=10306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91101287; PubMed=1846198;
 RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
 RA Silverstein S., Wagner E.K.;
 RT "Analysis of the herpes simplex virus type 1 promoter controlling the
 RT expression of UL38, a true late gene involved in capsid assembly.";
 RL J. Virol. 65:769-786(1991).
 CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
 CC EMBEDDED. BINDS DNA.
 CC -!- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M57646; AAA45830.1; -;
 KW Capsid assembly; Coat protein; DNA-binding.
 FT NON_TER
 FT 6
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;
 Query Match 36.7%; Score 11; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 pl 2
 Db 5 PL 6
 RESULT 3
 ACHI_ACHFU
 ID ACHI_ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ACHATIN-I.
 OS Achatina fullica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=FERUSSAC; TISSUE=Ganglion;
 RX MEDLINE=89273551; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fullica Ferussac containing a D-amino acid residue";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN=FERUSSAC; TISSUE=Heart atrium;
 RX MEDLINE=91264856; PubMed=1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fullica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=93014529; PubMed=1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;

RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RL D-amino acid residue.";
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -!- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (FON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 DR PIR: A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2 D-PHENYLALANINE.
 FT SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
 Query Match 33.3%; Score 10; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 3 gla 5
 Db 1 GLA 3
 RESULT 4
 AL14_CARMA
 ID AL14_CARMA STANDARD; PRT; 5 AA.
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CARCINUSTATIN 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 5 5 AMIDATION (POTENTIAL).
 FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
 Query Match 33.3%; Score 10; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 gl 4
 Db 4 GL 5
 RESULT 5
 TMOF_SARBU
 ID TMOF_SARBU STANDARD; PRT; 6 AA.
 AC P41495.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE TRYPSTIN-MODULATING OOSTATIC FACTOR (TMOF).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.

OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807;
 RA Byllemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 RA de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic
 RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 RT (Sarcophaga) bullata";
 RL Regul. Pept. 50:61-72(1994).
 CC -!- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
 CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
 CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 CC DEVELOPMENT.
 CC -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
 CC EPITHELIUM AFTER A BLOOD MEAL.
 KW Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 33.3%; Score 10; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05; 2; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0;

Qy 1 plgl 4
 I
 I
 Db 2 PTNL 5

RESULT 6
 CIP1_MYPED
 ID CIP1_MYPED STANDARD; PRT; 6 AA.
 AC P13736;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CONTRACTION-INHIBITING PEPTIDE I (MIP I).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP II.
 DR PIR: A27696; A27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 30.0%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0;

Qy 1 pl 2
 I
 I
 Db 3 PM 4

RESULT 7
 CIP2_MYPED
 ID CIP2_MYPED STANDARD; PRT; 6 AA.
 AC P13737;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CONTRACTION-INHIBITING PEPTIDE II (MIP II).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilus.
 OX NCBI_TaxID=6550;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=88240357; PubMed=3377776;
 RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
 RT "Structures and actions of Mytilus inhibitory peptides";
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- SIMILARITY: TO MIP I.
 DR PIR: B27696; B27696.
 KW Hormone; Amidation.
 FT MOD_RES 6 AMIDATION.
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 30.0%; Score 9; DB 1; Length 6;
 Best Local Similarity 50.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0;

Qy 1 pl 2
 I
 I
 Db 3 PM 4

RESULT 8
 DCML_PSECH
 ID DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pedal ganglion;
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
 CC MUSCLES.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
 CC ACCEPTOR.
 CC -!- COFACTOR: MOLYBDENUM.
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR: PL0140; PL0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 4;
 Best Local Similarity 50.0%; Pred. No. 1e+05; 0; Indels 0; Gaps 0;
 Matches 1; Conservative 1; Mismatches 0;

Qy 2 lq 3
 I
 I
 Db 1 MG 2

RESULT 9
 DCMS_PSECH
 ID DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;

```

DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=290;
RN [1]
RN SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of Co dehydrogenase structural genes in
  carboxydohydrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
  ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
  SMALL.
DR PIR; PLO146; PLO146.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 4;
Best Local Similarity 33.3%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 lar 6
DB 1 MAK 3

RESULT 10
UF01_MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P19) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE.
RP TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
  using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
  NON_TER 5
FT PROTEIN IS: 6.6, ITS MW IS: 19 KDA.
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 26.7%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3
DB 2 IG 3

RESULT 11
THYL_PIG STANDARD; PRT; 3 AA.
ID THYL_PIG
AC P01151.

```

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE THYROLIBERIN (THYROTROPIN RELEASING HORMONE) (TRH).
OS Sus scrofa (Pig); Ovis aries (Sheep);
OS Bombina orientalis (Oriental fire-bellied toad), and
OC Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RN SEQUENCE.
RP SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106(1970).
RN [2]
RN SEQUENCE.
RP SPECIES=Pig;
RX MEDLINE=70039904; PubMed=4982117;
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
  releasing hormone and pyroglutamyl-histidyl-proline amide.";
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RN SEQUENCE.
RP SPECIES=Sheep; TISSUE=Hypothalamus;
RX Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
  Ward D.N.;
RA "The elucidation of the primary structure of the hypothalamic thyrold
  stimulating hormone releasing factor of ovine origin by means of mass
  spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]
RN SEQUENCE.
RP SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
  Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic
  TSH-releasing factor.";
RL Nature 226:321-325(1970).
RN [5]
RN SEQUENCE.
RP SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RN SEQUENCE.
RP SPECIES=N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
  viridescens) brain in vitro. Isolation and characterization of
  thyrotropin releasing factor.";
RL J. Neurochem. 23:471-478(1974).
CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
  IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
  NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
CC PIR; A01415; RHPGT.
DR PIR; A93750; RHSHT.
DR PIR; A90919; RHTDFO.
DR PIR; A92971; A92971.
KW Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 3 3 AMIDATION.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 3;

```

```

Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
   |
Db 3 p 3

RESULT 12
EESI_HUMAN
ID EESI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSINOPHILOTACTIC PEPTIDES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotactic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -!- MISCELLANEOUS; THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
DR PTR: A03190; ETHUL.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
/FTID=VAR_005201.
SQ SEQUENCE 4 AA; 390 MW; 6805B862A0000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. le+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3
   |
Db 1 VG 2

RESULT 13
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L1 (YML1) (FRAGMENT).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria."
RT FEBS Lett. 284:51-56(1991).
DR PIR: S17255; S17255.
DR SGD: L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4 4

Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
   |
Db 4 p 4

RESULT 14
TUFT_HUMAN
ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFTSIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS; AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR: A02147; A02147.
DR MIM: 191150; -.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. le+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
   |
Db 3 p 3

RESULT 15
BPP7_BOTIN
ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]

```

RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RL peptides from Bothrops insularis snake venom.";
 CC J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR; G37196; G37196.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 23.3%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 p 1
 Db 5 p 5

Search completed: February 28, 2002, 16:54:52
 Job time: 212 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:51:05 ; Search time 22.14 Seconds
(without alignments)
39.640 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 13

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	9	30.0	5	13	P82099 litoria rub
2	9	30.0	6	13	P82096 litoria rub
3	8	26.7	6	10	P82181 spinacia ol
4	8	26.7	6	10	P82182 spinacia ol
5	7	23.3	5	13	P82073 litoria rub
6	6	20.0	5	10	Q99007 hordeum vul
7	5	16.7	6	10	P82541 spinacia ol
8	4	13.3	4	11	Q08433 rattus norv
9	4	13.3	5	13	P82070 litoria rub
10	4	13.3	5	13	P82071 litoria rub
11	4	13.3	6	4	Q08720 homo sapien
12	2	6.7	5	13	P82072 litoria rub
13	2	6.7	5	13	P82100 litoria rub

ALIGNMENTS

RESULT 1

```
P82099 ID P82099 PRELIMINARY; PRT; 5 AA.
AC P82099;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ELECTRN 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 30.0%; Score 9; DB 13; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2
Db 4 PM 5

RESULT 2
P82096 ID P82096 PRELIMINARY; PRT; 6 AA.
AC P82096;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE ELECTRN 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litori electrica. Comparison with the skin peptides from Litoria
RT rubella."
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 30.0%; Score 9; DB 13; Length 6;
Best Local Similarity 50.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2
Db 3 PI 4

RESULT 3
P82181 ID P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
```

DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 BETA (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal_L10.
 DR InterPro: IPR002363; Ribosomal_L10_eub.
 DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

 Query Match 26.7%; Score 8; DB 10; Length 6;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 4 lar 6
 : :
 DB 2 ISR 4

 RESULT 4
 P82182
 ID P82182 PRELIMINARY; PRT; 6 AA.
 AC P82182;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHLOROPLAST 50S RIBOSOMAL PROTEIN L10 GAMMA (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435798; PubMed=10874046;
 RA Yamaguchi K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal_L10.
 DR InterPro: IPR002363; Ribosomal_L10_eub.
 DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 26.7%; Score 8; DB 10; Length 6;
 Best Local Similarity 33.3%; Pred. No. 4.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 4 lar 6
 : :
 DB 2 ISR 4

 RESULT 5
 P82073
 ID P82073 PRELIMINARY; PRT; 5 AA.
 AC P82073;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RUBELLIDIN 3.2.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella.";
 RL Aust. J. Chem. 52:0-0(1999).
 CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

 Query Match 23.3%; Score 7; DB 13; Length 5;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 2 lg 3
 : :
 DB 1 VG 2

 RESULT 6
 Q99007
 ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC Q99007;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
 GN AMYL.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers.";
 RL Plant Mol. Biol. 16:713-721(1991).
 CC -!- CATALYTIC ACTIVITY: ENDHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR EMBL: X54643; CAA38455.1; -.
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 20.0%; Score 6; DB 10; Length 5;
 Best Local Similarity 50.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 la 5
 : 1
 Db 1 MA 2

RESULT 7
 P82541 ID P82541 PRELIMINARY; PRT; 6 AA.
 AC P82541:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CHLOROPLAST 30S RIBOSOMAL PROTEIN S19 BETA (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALVARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 37:28455-28465(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
 CC -1- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
 CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
 CC FORM IS THE MINOR BASIC FORM.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR002222; Ribosomal_S19.
 DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
 DR PRINTS: PR00975; RIBOSOMALS19; PARTIAL.
 DR PROSITE: PS00323; RIBOSOMALS19; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6 6
 SQ SEQUENCE 6 AA; 732 MW; 6333735A411C0000 CRC64;

Query Match 16.7%; Score 5; DB 10; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 r 6
 : 1
 Db 2 R 2

RESULT 8
 Q08433 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC Q08433:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE, MICROSOMAL (EC 2.4.1.17) (UDP-GT)
 DE (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GUNN;
 RX MEDLINE=91282756; PubMed=1840486;
 RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 RT hyperbilirubinemic Gunn rat.";
 RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
 CC -1- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
 CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
 CC ENDOGENOUS COMPOUNDS.
 CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 CC -1- SUBCELLULAR LOCATION: MICROSOME.
 DR EMBL: S38636; AAB19259.1; -.
 KW Transferase; Glycosyltransferase; Microsome; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 13.3%; Score 4; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 l 2
 : 1
 Db 3 L 3

RESULT 9
 P82070 ID P82070 PRELIMINARY; PRT; 5 AA.
 AC P82070:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RUBELLIDIN 1.1
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE=SKIN SECRETION;
 RA Steinhilber S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella', the skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -1- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -1- MASS SPECTROMETRY: MW=598; METHOD=FAB.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 a 5

```
Db 5 A 5
RESULT 10
P82071 ID P82071 PRELIMINARY; PRT; 5 AA.
AC P82071;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTI-BIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 13.3%; Score 4; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 A 5
Db 5 A 5

RESULT 11
Q08720 ID Q08720 PRELIMINARY; PRT; 6 AA.
AC Q08720;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Y PROTEIN (FRAGMENT).
GN CREB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010691; PubMed=1396344;
RA Waeber G., Habener J.F.;
RT "Novel testis germ cell-specific transcript of the CREB gene contains
RT an alternatively spliced exon with multiple in-frame stop codons.";
RL Endocrinology 131:2010-2015(1992).
DR EMBL; X68994; CAA48780.1;
FT NON_TER 1 1
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 695 MW; 67272EB9C735D000 CRC64;

Query Match 13.3%; Score 4; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 1 2
Db 2 L 2

RESULT 12
P82072 ID P82072 PRELIMINARY; PRT; 5 AA.
AC P82072;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
CC ANTI-BIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
FT SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 6.7%; Score 2; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1 2
Db 1 I 1

RESULT 13
P82100 ID P82100 PRELIMINARY; PRT; 5 AA.
AC P82100;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE ELECTRIN 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:0-0(1999).
KW Amphibian skin; Amidation.
FT MOD_RES 5 5
FT SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 6.7%; Score 2; DB 13; Length 5;
Best Local Similarity 0.0%; Pred. No. 4.7e+05;
```

Matches	0;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	2	1	2						
Db	2	1	2						

Search completed: February 28, 2002, 16:54:35
Job time: 210 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:47:45 ; Search time 23.61 Seconds
(without alignments)
18.824 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 plglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 34718

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101.*

1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	18 AAB74602	3-methylcholanthrene
2	30	100.0	6	19 AAW52139	Matrix metallopro
3	25	83.3	6	5 AAP40807	Sequence of synthe
4	25	83.3	6	21 AAB01559	Collagenase substr
5	23	76.7	6	20 AAY31035	Non-crosslinked pr
6	23	76.7	6	21 AAB10447	Peptide sequencing
7	23	76.7	6	21 AAB01557	Collagenase substr
8	21	70.0	4	4 AAP30449	Substrate for coll
9	21	70.0	4	4 AAP30450	Peptide conjugated
10	21	70.0	4	19 AAW51622	Peptide-lipid con
11	21	70.0	4	22 AAB62798	

12	21	70.0	6	5 AAP40806	Sequence of synthe
13	21	70.0	6	18 AAW24981	Recombinant human
14	21	70.0	6	21 AAB37325	Peptide linker #10
15	21	70.0	6	21 AAB15681	Matrix metalloprot
16	21	70.0	6	21 AAB22834	Matrix metalloprot
17	21	70.0	6	21 AAB23852	Thiopeptolide subs
18	21	70.0	6	21 AAB01558	Collagenase substr
19	21	70.0	6	22 AAB67721	Amino acid sequenc
20	21	70.0	6	22 AAB67722	Amino acid sequenc
21	21	70.0	6	22 AAB73911	MMP-2 protease cle
22	21	70.0	6	22 AAB73912	MMP-2 protease cle
23	21	70.0	6	22 AAB70300	Thiopeptolide subs
24	21	70.0	6	22 AAB74620	Thiopeptolide amin
25	21	70.0	6	22 AAB68684	Thiopeptolide. Un
26	21	70.0	6	22 AAB60147	Matrix metalloprot
27	21	70.0	6	22 AAB35976	Collagenase cleava
28	19	63.3	5	15 AAR53408	Peptide having opi
29	19	63.3	6	15 AAR64010	C5a anaphylatoxin-
30	19	63.3	6	20 AAW94401	Immobilised peptid
31	19	63.3	6	21 AAB01556	Collagenase substr
32	19	63.3	6	22 AAB86393	Collagenase derive
33	18	60.0	6	5 AAP40580	Sequence of peptid
34	18	60.0	6	18 AAW17696	Substrate #1 for m
35	18	60.0	6	20 AAY01259	Peptide #2 charact
36	18	60.0	6	21 AAB12385	Collagenase derive
37	18	60.0	6	22 AAB86398	Collagenase derive
38	17	56.7	3	22 AAB90861	Melanocyte stimula
39	17	56.7	4	2 AAP10467	Peptide for use in
40	17	56.7	4	2 AAP10273	Enzyme activity de
41	17	56.7	4	3 AAP20330	Insulin and secret
42	17	56.7	4	4 AAP30451	Substrate for coll
43	17	56.7	4	6 AAP50806	Sequence of the re
44	17	56.7	4	16 AAR98901	Melanotrophic rele
45	17	56.7	4	16 AAR98903	Melanotrophic rele

ALIGNMENTS

RESULT	1
AAB74602	
ID	AAB74602 standard; peptide: 6 AA.
XX	AAB74602;
XX	AC
XX	21-MAY-2001 (first entry)
XX	3-methylcholanthrene (MCA) peptide substrate.
XX	3-methylcholanthrene; MCA; substrate; metalloproteinase inhibitor;
KW	cancer; metastasis; arthritis.
XX	Synthetic.
OS	Synthetic.
XX	Key
XX	Location/Qualifiers
FT	Modified-site 1
FT	/note= "Pro in N-terminally modified to
FT	7-methoxycoumarin-4-yl-acetyl-pro"
FT	Modified-site 5
FT	/note= "Ala is N-terminally modified to
FT	3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl-ala"
FT	Modified-site 6
FT	/note= "amidated"
XX	WO9720824-A1.
PN	12-JUN-1997.
XX	05-DEC-1996; 96WO-US19328.
XX	08-DEC-1995; 95US-0569766.
XX	(AGOU-) AGOURON PHARM INC.

XX Zook SE, Dagnino R, Deason ME, Bender SL, Melnick MJ;
 XX WPI; 1997-332465/30.
 XX
 PT New N-hydroxy-benzenesulphonyl carboxamide derivatives - are
 PT metallo-protease inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 XX Example 22; Page 108; 151pp; English.
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. N-hydroxy benzenesulphonyl (thiazine or piperazine)
 CC carboxamide derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 DB 1 piglar 6
 RESULT 2
 AAW52139
 ID AAW52139 standard; Peptide; 6 AA.
 XX
 XX AAW52139;
 XX
 DT 20-JUL-1998 (first entry)
 XX
 DE Matrix metalloproteinase MMP-9 substrate B.
 XX
 KW Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;
 KW metalloproteinase 12; MMP-12; osteoclastic proteinase;
 KW osteoclast; inhibitor; metabolic bone disease; osteoporosis;
 KW bone resorption; metastasis; tumour; cancer; ulcer; arthritis;
 KW periodontal disease; therapy.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Mca-proline"
 FT Cleavage-site 3..4
 FT Modified-site 5
 FT /note= "Dpa-alanine"
 XX
 PN WO9804287-A1.
 XX
 XX 05-FEB-1998.
 XX
 XX 29-JUL-1997; 97WO-EP04110.
 XX
 XX 30-JUL-1996; 96GB-0015976.
 XX
 PA (CLIN-) CENT CLINICAL & BASIC RES.
 XX
 PI Delaisse J, Foged NT, Meldal M;
 XX
 XX WPI; 1998-130425/12.
 XX
 PT Use of inhibitors of protease(s) involved in osteoclast activity -

PT useful for, e.g. treating metabolic bone disease such as
 PT osteoporosis
 XX
 XX Example 6b; Page 44; 110pp; English.
 XX
 CC Peptide B is a substrate of matrix metalloproteinase MMP-9. Novel
 CC peptide substrate mimicking MMP-inhibitors (see AAW52132-33) are
 CC promising agents for use in treatment of bone metabolic disease.
 CC They can be used to inhibit proteinases involved in the
 CC recruitment, proliferation, differentiation or migration of
 CC osteoclast precursor cells or in the migration, fusion, attachment,
 CC polarisation, removal of mineralised osseous substance or death of
 CC osteoclasts. The inhibitors reduce the rate of bone resorption
 CC and are used to treat or prevent, e.g. osteoporosis and osteolytic
 CC bone metastases. They are also useful in, e.g. treatment of
 CC cancer, ulcers, arthritis and periodontal disease.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 30; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 piglar 6
 DB 1 piglar 6
 RESULT 3
 AAP40807
 ID AAP40807 standard; Protein; 6 AA.
 XX
 XX AAP40807;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Sequence of synthetic peptide substrate for mammalian collagenase.
 XX
 KW Collagenase; proteolytic enzyme; collagen; protein.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /label= Ac-P
 FT Modified-site 6
 FT /label= G-OGH2CH3
 XX
 PN GB2131813-A.
 XX
 XX 27-JUN-1984.
 XX
 XX 15-DEC-1983; 83GB-0033460.
 XX
 PR 16-DEC-1982; 82US-0450318.
 PR 16-MAR-1984; 84US-0590395.
 XX
 XX (MONS) MONSANTO CO.
 PA (MAUS/) MONSANTO CO.
 XX
 XX Weingarten HI;
 XX
 XX WPI; 1984-160555/26.
 XX
 PT Diagnostic hexa:peptide substrate - for determining collagenase
 PT in biological samples
 XX
 XX Claim 3; Page 6; 6pp; English.
 XX
 CC The inventors claim synthetic peptide substrates having high
 CC activity for the enzyme collagenase. The G-L peptide bond (AAs 3-4)
 CC in the peptides of the invention cleaves substantially more readily
 CC with mammalian collagenase than the G-I peptide in the corresponding
 CC posn. of existing peptides. It has also been found that the G-L-L

CC sequence is further rate enhancing in the cleavage reaction with
 CC mammalian collagenase. Thus the peptides of this invention are 2-1/2
 CC times as active as the corresponding peptides contg. the G-I-L
 CC sequence in the same posn.
 XX
 SQ Sequence 6 AA;

Query Match 83.3%; Score 25; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgla 5
 |||||
 Db 1 plgla 5

RESULT 4
 AAB01559
 ID AAB01559 standard; peptide: 6 AA.
 AC AAB01559;
 XX
 XX 08-NOV-2000 (first entry)

DT Collagenase substrate site found in collagen.

DE Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
 KW sealant; tissue engineering; wound healing; scaffold;
 KW cell transplant; adhesion prevention; cell migration; collagenase;
 KW plasmin; elastase.

XX Homo sapiens.

XX WO200044808-A1.

XX 03-AUG-2000.

XX 01-FEB-2000; 2000WO-US02608.

XX 01-FEB-1999; 99US-0118093.

XX (HUBB/) HUBBELL J A.

XX Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;
 PI Tirelli N, Vernon B;
 XX
 XX WPI: 2000-524289/47.

XX Producing polymeric biomaterials by polymerizing two or more precursor
 PT components (e.g. polymer, protein or peptide) of the biomaterial,
 PT useful for delivering therapeutic molecules to a subject and as
 PT adhesives or sealants
 XX

PS Disclosure: Page 45; 119pp; English.

XX A method of making polymeric biomaterials is described comprising
 CC combining two or more precursor components (e.g. polymer, protein or
 CC peptide) of the biomaterial under conditions that allow
 CC polymerisation of the two components. Polymerisation occurs through
 CC self selective reaction between a strong nucleophile and a conjugated
 CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
 CC addition. The polymeric hydrogels can be used in a variety of
 CC applications. They can be used to deliver therapeutic molecules to
 CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
 CC lung), as tissue engineering and wound healing scaffolds, and as cell
 CC transplant devices. The biomaterials are also useful for adhesion
 CC prevention to minimise unwanted operative or post-traumatic adhesions.
 CC In the instances where the precursor for the polymeric biomaterial
 CC is a peptide, the nucleophile is the amino acid cysteine. This
 CC results in peptides of structure similar to H₂N-CXXXXXXC-COOH
 CC (See GENESQ records AAB01531-B01535). The length of XXXXX is variable
 CC and can be of any number. It is particularly useful when the

CC sequences in the domains shown as XXXXX are substrates for enzymes
 CC that are involved in cell migration (e.g. as substrates for enzymes
 CC such as collagenase, plasmin or elastase).
 XX
 SQ Sequence 6 AA;

Query Match 83.3%; Score 25; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgla 5
 |||||
 Db 1 plgla 5

RESULT 5
 AAY31035
 ID AAY31035 standard; peptide: 6 AA.
 AC AAY31035;
 XX
 XX 21-OCT-1999 (first entry)

DT Non-crosslinked protein particle peptide 84.

DE Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; nanometer; micrometer; clearance.
 KW Synthetic.

XX US5945033-A.

XX 31-AUG-1999.

XX 12-NOV-1996; 96US-0747137.

XX 14-MAR-1994; 94US-0212546.

XX 15-JAN-1991; 91US-0641720.

XX 13-OCT-1992; 92US-0859560.

XX 01-JUN-1993; 93US-0069831.

XX 12-NOV-1996; 96US-0747137.

XX (HEMO-) HEMOSPHERE INC.

XX Yen RCK;

XX WPI: 1999-508153/42.

XX Non-crosslinked protein particles for therapeutic and diagnostic use
 XX
 XX Example 22; Column 83-84; 65pp; English.

XX This invention describes a novel aqueous suspension of monodisperse
 CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
 CC is stable against dissolving upon dilution with an alcohol-free aqueous
 CC medium. The method involves (a) forming an aqueous solution containing
 CC albumin and hemoglobin and (b) treating the aqueous solution with an
 CC alcohol to cause the solution to become turbid. The particles are useful
 CC as agents for in vivo administration, either of their own administration
 CC or as a vehicle for other therapeutic or diagnostic agents. The method
 CC permits the formation of albumin and hemoglobin particles in the
 CC nanometer and micrometer size range, in a form closer to their natural
 CC form than the forms of the prior art. The particles therefore constitute
 CC a more closely controlled agent for in vivo administration, with greater
 CC ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.

XX Sequence 6 AA;

Query Match 76.7%; Score 23; DB 20; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 lglar 6
|||||

Db 2 lglar 6
|||||

RESULT 6
AAB10447
ID AAB10447 standard; peptide; 6 AA.
XX
AC AAB10447;
XX
DT 01-DEC-2000 (first entry)
XX
DE Peptide sequencing method synthetic peptide SEQ ID NO: 3.
XX
KW Peptide sequencing; fragmentation pattern; amino acid modification;
KW post-translational modification; laundry; cleansing product; proteomic;
KW y-ion.
XX
OS Synthetic.
XX
PN WO200043792-A2.
XX
PD 27-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-US00790.
XX
PR 20-JAN-1999; 99US-0116502.
PR 29-SEP-1999; 99US-0156677.
XX
PA (PROC) PROCTER & GAMBLE CO.
XX
PI Keough TW, Youngquist RS;
XX
DR WPI; 2000-543265/49.
XX
PT Determining amino acid sequence of polypeptide by derivatizing the
PT N-terminus of the polypeptide with acidic moieties, analyzing
PT derivatized products using mass spectrometric technique and
PT interpreting the fragmentation pattern -
XX
PS Example 4; Page 29; 30pp; English.
XX
CC This invention describes a novel method for determining the amino acid
CC sequence of a polypeptide comprising derivatizing the N-terminus of the
CC polypeptide or polypeptides with one or more acidic moieties with pK_a of
CC less than 2 when coupled with the polypeptide or polypeptides, analyzing
CC the derivatized products using a mass spectrometric technique to provide
CC a fragmentation pattern free of a- and b-ions and interpreting the
CC fragmentation pattern. The method is used for sequencing wild-type or
CC variant polypeptides. Applications include biological studies,
CC identification of post-translational modifications in proteins,
CC identification of amino acid modifications in variant proteins used in
CC e.g. commercial laundry and cleansing products, designing oligonucleotide
CC probes for gene cloning, rapid characterization of products formed in
CC directed evolution studies, combinatorial chemistry and peptide libraries
CC and proteomics. Derivatization of the polypeptides with acid groups gives
CC almost exclusive y-ion fragmentation and very little a-ion and b-ion
CC 'noise', providing mass spectra which are more easily interpreted. The
CC method is simple, efficient and widely applicable to both wild-type and
CC variant polypeptides. This sequence represents a synthetic peptide used
CC to illustrate the method of the invention.
XX
SQ Sequence 6 AA;

Query Match 76.7%; Score 23; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 lglar 6
|||||

Db |||||
2 lglar 6

RESULT 7
AAB01557
ID AAB01557 standard; peptide; 6 AA.
XX
AC AAB01557;
XX
DT 08-NOV-2000 (first entry)
XX
DE Collagenase substrate site found in collagen.
XX
KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
KW sealant; tissue engineering; wound healing; scaffold;
KW cell transplant; adhesion prevention; cell migration; collagenase;
KW plasmin; elastase.
XX
OS Homo sapiens.
XX
PN WO200044808-A1.
XX
PD 03-AUG-2000.
XX
PF 01-FEB-2000; 2000WO-US02608.
XX
PR 01-FEB-1999; 99US-0118093.
XX
PA (HUBB/) HUBBELL J A.
XX
PI Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;
PI Tirelli N, Vernon B;
XX
DR WPI; 2000-524289/47.
XX
PT Producing polymeric biomaterials by polymerizing two or more precursor
PT components (e.g. polymer, protein or peptide) of the biomaterial,
PT useful for delivering therapeutic molecules to a subject and as
PT adhesives or sealants
XX
PS Disclosure; Page 45; 119pp; English.
XX
CC A method of making polymeric biomaterials is described comprising
CC combining two or more precursor components (e.g. polymer, protein or
CC peptide) of the biomaterial under conditions that allow
CC polymerisation of the two components. Polymerisation occurs through
CC self selective reaction between a strong nucleophile and a conjugated
CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
CC addition. The polymeric hydrogels can be used in a variety of
CC applications. They can be used to deliver therapeutic molecules to
CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
CC lung), as tissue engineering and wound healing scaffolds, and as cell
CC transplant devices. The biomaterials are also useful for adhesion
CC prevention to minimise unwanted operative or post-traumatic adhesions.
CC In the instances where the precursor for the polymeric biomaterial
CC is a peptide, the nucleophile is the amino acid cysteine. This
CC results in peptides of structure similar to H₂N-CXXXXXXC-COOH
CC (See GENESQ records AAB01531-B01535). The length of XXXX is variable
CC and can be of any number. It is particularly useful when the
CC sequences in the domains shown as XXXX are substrates for enzymes
CC that are involved in cell migration (e.g. as substrates for enzymes
CC such as collagenase, plasmin or elastase).
XX
SQ Sequence 6 AA;

Query Match 76.7%; Score 23; DB 21; Length 6;
Best Local Similarity 80.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 lglar 5
|||||

Db 1 plgl 5

RESULT 8

AAP30449
ID AAP30449 standard; peptide; 4 AA.XX
AC AAP30449;

XX 04-SEP-1992 (first entry)

DT Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX Substrate for collagenase.

XX Peptide; peptolide; cleavage.

XX Synthetic.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```

PD 23-APR-1998.
XX
XX PF 15-OCT-1997; 97WO-US18538.
XX
XX PR 15-OCT-1996; 96US-0027544.
XX
XX (LIPO ) LIPOSOME CO INC.
XX
XX PI Ali S, Cabral-Lilly D, Erukulla RK, Franklin JC;
XX PI Janoff AS, Meers PR, Pak C;
XX
XX WPI; 1998-261025/23.
XX
XX New peptide-lipid conjugates are incorporated into liposome(s) - to
XX PT selectively destabilise the liposome(s) in the vicinity of target
XX PT peptidase-secreting cells, e.g., tumour cells; useful in diagnosis
XX PT and therapy
XX
XX PS Claim 8; Page 33; 55pp; English.
XX
XX CC The invention relates to peptide-lipid conjugates and their use in
XX CC the preparation of liposomes which are predisposed to degradation in the
XX CC presence of peptidase-secreting cells and hence are targeted to these
XX CC cells. The liposomes can be used to treat mammalian diseases, disorders
XX CC and conditions, e.g. tumours, microbial infections and inflammation. The
XX CC liposomes allow selective delivery of an active agent to desired cells.
XX CC The liposomes are stable when the peptide remains conjugated to the
XX CC lipid. However, once the peptide portion of the conjugate is cleaved
XX CC from the lipid, by the action of cell-secreted peptidases, the liposomes
XX CC destabilise and release their contents in the vicinity of, or into, the
XX CC secreting cells. The liposomes can thus be used to treat conditions
XX CC characterised by the occurrence of peptidase-secreting cells. For
XX CC example, the breast cancer cell line MCF-7 is known to secrete elastase,
XX CC the levels of which are inversely correlated to overall survival in
XX CC breast cancer patients. The present sequence represents a specifically
XX CC claimed peptide which forms part of the peptide-lipid conjugate.
XX
XX SQ Sequence 4 AA;

Query Match 70.0%; Score 21; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plql 4
Db 1 plql 4

RESULT 11
AAB62798
ID AAB62798 standard; peptide; 4 AA.
XX
XX AC AAB62798;
XX
XX DT 03-APR-2001 (first entry)
XX
XX DE Peptide-lipid conjugate peptide #13.
XX
XX KW Peptide-lipid conjugate; liposome; liposomal drug delivery; cancer;
XX KW peptidase-secreting cell; phosphatidylethanolamine;
XX KW inflammatory disorder; neuropathy.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /label= OTHER
XX FT /note= "optionally modified by methoxysuccinyl or
XX FT succinyl group"
XX FT Modified-site 4
XX FT /label= OTHER
XX FT /note= "C-terminal phosphatidylethanolamine"
XX

PD 23-APR-1998.
XX
XX PF 15-OCT-1997; 97WO-US18538.
XX
XX PR 15-OCT-1996; 96US-0027544.
XX
XX (LIPO ) LIPOSOME CO INC.
XX
XX PI Ali S, Cabral-Lilly D, Erukulla RK, Franklin JC;
XX PI Janoff AS, Meers PR, Pak C;
XX
XX WPI; 1998-261025/23.
XX
XX New peptide-lipid conjugates are incorporated into liposome(s) - to
XX PT selectively destabilise the liposome(s) in the vicinity of target
XX PT peptidase-secreting cells, e.g., tumour cells; useful in diagnosis
XX PT and therapy
XX
XX PS Claim 8; Page 33; 55pp; English.
XX
XX CC The invention relates to peptide-lipid conjugates and their use in
XX CC the preparation of liposomes which are predisposed to degradation in the
XX CC presence of peptidase-secreting cells and hence are targeted to these
XX CC cells. The liposomes can be used to treat mammalian diseases, disorders
XX CC and conditions, e.g. tumours, microbial infections and inflammation. The
XX CC liposomes allow selective delivery of an active agent to desired cells.
XX CC The liposomes are stable when the peptide remains conjugated to the
XX CC lipid. However, once the peptide portion of the conjugate is cleaved
XX CC from the lipid, by the action of cell-secreted peptidases, the liposomes
XX CC destabilise and release their contents in the vicinity of, or into, the
XX CC secreting cells. The liposomes can thus be used to treat conditions
XX CC characterised by the occurrence of peptidase-secreting cells. For
XX CC example, the breast cancer cell line MCF-7 is known to secrete elastase,
XX CC the levels of which are inversely correlated to overall survival in
XX CC breast cancer patients. The present sequence represents a specifically
XX CC claimed peptide which forms part of the peptide-lipid conjugate.
XX
XX SQ Sequence 4 AA;

Query Match 70.0%; Score 21; DB 19; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plql 4
Db 1 plql 4

RESULT 12
AAP40806
ID AAP40806 standard; peptide; 6 AA.
XX
XX AC AAP40806;
XX
XX DT 29-JUL-1992 (first entry)
XX
XX DE Sequence of synthetic peptide substrate for mammalian collagenase.
XX
XX KW Collagenase; proteolytic enzyme; collagen; protein.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /label= Ac-P
XX FT Modified-site 6
XX FT /label= G-OCH2CH3
XX
XX PW GB2131813-A.
XX
XX DT 27-JUN-1984.
XX
XX PF 15-DEC-1983; 83GB-0033460.
XX
XX PR 16-DEC-1982; 82US-0450318.
XX PR 16-MAR-1984; 84US-0590395.
XX
XX (MONS ) MONSANTO CO.
XX PA (MAUS/) MONSANTO CO.
XX
XX PI Weingarten HI;
XX

```

DR WPI; 1984-160555/26.
 XX Diagnostic hexa-peptide substrate - for determining collagenase
 PT in biological samples
 PS Claim 2; Page 6; 6pp; English.
 XX The inventors claim synthetic peptide substrates having high
 CC activity for the enzyme collagenase. The G-L peptide bond (AAs 3-4)
 CC in the peptides of the invention cleaves substantially more readily
 CC with mammalian collagenase than the G-I peptide in the corresponding
 CC posn. of existing peptides. It has also been found that the G-L-L
 CC sequence is further rate enhancing in the cleavage reaction with
 CC mammalian collagenase. Thus the peptides of this invention are 2-1/2
 CC times as active as the corresponding peptides contg. the G-I-L
 CC sequence in the same posn.
 XX Sequence 6 AA;
 SQ

Query Match 70.0%; Score 21; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

RESULT 13
 AAW24981
 ID AAW24981 standard; peptide: 6 AA.
 AC AAW24981;
 XX
 DT 03-DEC-1997 (first entry)
 DE Recombinant human gelatinase thiopeptolide substrate.
 XX Catalytic domain; human; gelatinase; matrix metalloprotease; propeptide;
 KW hemopexin; fibronectin; vector; recombinant; deletion; hernia; joint;
 KW vertebral disc; dermal ulcer; scar tissue.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "acetylated N-terminus"
 FT
 FT Misc-difference 3..4
 FT /note= "amino acid residues linked by thioester bond"
 FT Modified-site 6
 FT /note= "Gly-OEt"
 XX
 PN US5646027-A.
 XX
 XX 08-JUL-1997.
 PD
 XX
 XX 08-SEP-1994; 94US-0303270.
 PF
 XX 08-SEP-1994; 94US-0303270.
 XX
 PR (WARN) WARNER LAMBERT CO.
 XX
 XX Hupe DJ, Johnson LL, Ye Q;
 PI WPI; 1997-362935/33.
 DR
 XX Production of recombinant human gelatinase catalytic domain protein
 PT - especially using vector containing new synthetic coding sequence
 XX
 XX Example 3; Column 10; 2lpp; English.
 PS
 XX This peptide is a substrate for a novel recombinant catalytic domain of

CC the human 72 kD gelatinase, a member of the matrix metalloprotease
 CC family, lacking its propeptide, C-terminal hemopexin-like domain or
 CC fibronectin-like insert (AAW24980). The catalytic domain protein is
 CC useful for treating herniated vertebral discs, treating dermal ulcers,
 CC modifying scar tissue formation and treating joint diseases.
 XX Sequence 6 AA;
 SQ

Query Match 70.0%; Score 21; DB 18; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

RESULT 14
 AAB37325
 ID AAB37325 standard; Peptide: 6 AA.
 XX
 AC AAB37325;
 XX
 DT 19-FEB-2001 (first entry)
 DE Peptide linker #10.
 XX Cytostatic; antiproliferative; vascular endothelial growth factor;
 KW VEGF; antibody; VEGF2 receptor; cancer; vascularised solid tumour;
 KW peptide linker.
 XX Unidentified.
 OS
 XX WO2000064946-A2.
 PN
 XX 02-NOV-2000.
 PD
 XX 28-APR-2000; 2000WO-US11367.
 PF
 XX 28-APR-1999; 99US-0131432.
 PR (TEXA) UNIV TEXAS SYSTEM.
 XX Thorpe PE, Brekken RA;
 PI WPI; 2000-687317/67.
 DR
 XX Immunogenic composition for the treatment and diagnosis of cancer
 PT comprises an anti-VEGF (vascular endothelial growth factor) antibody
 PT binding the same epitope as the monoclonal antibody ATCC PTA 1595 .
 XX
 PS Disclosure; Page 150; 298pp; English.
 XX
 XX The present invention relates to anti-vascular Endothelial Growth Factor
 CC (VEGF) antibodies that bind to the same epitope as the monoclonal
 CC antibody ATCC PTA 1595 and which significantly inhibit VEGF binding to
 CC the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF
 CC receptor VEGFR1. The present sequence is a peptide linker which can be
 CC used to link the antibodies of the present invention to anti-cellular or
 CC cytotoxic agents. The anti-VEGF antibodies of the present invention are
 CC useful for the treatment and diagnosis of cancer, especially vascularised
 CC solid tumours.
 XX Sequence 6 AA;
 SQ

Query Match 70.0%; Score 21; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
 Db 1 plgl 4
 ||||

Db 1 plgl 4

RESULT 15

AAB15681
ID AAB15681 standard; peptide; 6 AA.

XX AC AAB15681;

XX DT 08-JAN-2001 (first entry)

XX DE Matrix metalloprotease-sensitive linker peptide.

XX KW Matrix metalloprotease: MMP; restriction protease;

XX KW protease-sensitive linker; stabilon; stabilising fusion peptide;

XX KW single-chain antibody; vaccine; gene therapy;

XX KW protein degradation modulation; protein stability; Alzheimer's disease.

XX OS Unidentified.

XX PN WO200042185-A1.

XX PD 20-JUL-2000.

XX PF 11-JAN-2000; 2000WO-US00558.

XX PR 11-JAN-1999; 99US-0115505.

XX PA (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX PA (MCIN/) MCINNIS P A.

XX PI Chain DG;

XX WPI; 2000-476059/41.

DR PT Modulating degradability of protein or peptide useful for gene therapy
PT involving antibodies, comprises altering a gene at the N terminus to
PT render protein or peptide metabolically stable -
XX PS Disclosure; Page 12; 76pp; English.

XX CC The present sequence is a peptide which is sensitive to matrix
CC metalloprotease (MMP). It may be used to link a stabilising fusion
CC peptide, referred to as a stabilon, to the N-terminus of a single-chain
CC antibody. The stabilon increases stability of the antibody against
CC proteolysis in vivo. Induction of expression of MMP by means of an
CC inducible promoter causes cleavage of the linker and removal of the
CC stabilon. This renders the antibody susceptible to proteolysis by the
CC N-end rule pathway. Attachment of the stabilon to the antibody through a
CC protease-sensitive linker region therefore allows modulation of antibody
CC stability. Stabilised recombinant proteins may be used in gene therapy
CC for the treatment of disorders such as Alzheimer's disease.

XX SQ Sequence 6 AA;

Query Match 70.0%; Score 21; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4

Db 1 plgl 4

Search completed: February 28, 2002, 16:51:00
Job time: 195 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:50:15 ; Search time 90.37 seconds
(without alignments)
18.435 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 89186

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PTCUS_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/2/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/2/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/2/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/2/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/2/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/2/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/2/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/2/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/2/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/2/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/2/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/2/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/2/paa/US097_COMB.pep.*
22: /cgn2_6/ptodata/2/paa/US098_COMB.pep.*
23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	6	18	US-09-464-908-1
2	25	83.3	6	18	US-09-496-231A-31
3	25	83.3	6	22	US-09-808-832-75
4	23	76.7	6	18	US-09-496-231A-29
5	21	70.0	4	15	US-09-101-167-23
6	21	70.0	4	15	US-09-168-010-15
7	21	70.0	4	15	US-09-168-010-20
8	21	70.0	4	15	US-09-168-010-21
9	21	70.0	4	17	US-09-343-650-15
					Sequence 1, Appl
					Sequence 31, Appl
					Sequence 75, Appl
					Sequence 29, Appl
					Sequence 23, Appl
					Sequence 15, Appl
					Sequence 20, Appl
					Sequence 21, Appl
					Sequence 15, Appl

10	21	70.0	4	17	US-09-343-650-20	Sequence 20, Appl
11	21	70.0	4	17	US-09-343-650-21	Sequence 21, Appl
12	21	70.0	4	21	US-09-704-251-13	Sequence 13, Appl
13	21	70.0	4	22	US-09-808-832-203	Sequence 203, App
14	21	70.0	4	23	US-09-972-772-13	Sequence 13, Appl
15	21	70.0	5	22	US-09-808-832-8	Sequence 8, Appl
16	21	70.0	5	22	US-09-808-832-16	Sequence 16, Appl
17	21	70.0	5	22	US-09-808-832-205	Sequence 205, App
18	21	70.0	5	22	US-09-808-832-206	Sequence 206, App
19	21	70.0	6	13	US-08-909-601-34	Sequence 34, Appl
20	21	70.0	6	13	US-08-909-601-34	Sequence 34, Appl
21	21	70.0	6	13	US-08-909-607-34	Sequence 34, Appl
22	21	70.0	6	18	US-09-496-231A-30	Sequence 30, Appl
23	21	70.0	6	19	US-09-561-005-24	Sequence 24, Appl
24	21	70.0	6	19	US-09-561-108-24	Sequence 24, Appl
25	21	70.0	6	19	US-09-561-499-24	Sequence 24, Appl
26	21	70.0	6	19	US-09-561-500-24	Sequence 24, Appl
27	21	70.0	6	19	US-09-561-526-24	Sequence 24, Appl
28	21	70.0	6	19	US-09-562-245-24	Sequence 24, Appl
29	21	70.0	6	20	US-09-639-667-7	Sequence 7, Appl
30	21	70.0	6	20	US-09-640-198-9	Sequence 9, Appl
31	21	70.0	6	20	US-09-640-198-11	Sequence 11, Appl
32	21	70.0	6	21	US-09-753-078-3	Sequence 3, Appl
33	21	70.0	6	22	US-09-808-832-39	Sequence 39, Appl
34	21	70.0	6	22	US-09-808-832-52	Sequence 52, Appl
35	21	70.0	6	22	US-09-808-832-53	Sequence 53, Appl
36	21	70.0	6	22	US-09-808-832-54	Sequence 54, Appl
37	21	70.0	6	22	US-09-808-832-58	Sequence 58, Appl
38	21	70.0	6	22	US-09-808-832-59	Sequence 59, Appl
39	21	70.0	6	22	US-09-808-832-60	Sequence 60, Appl
40	21	70.0	6	22	US-09-808-832-61	Sequence 61, Appl
41	21	70.0	6	22	US-09-808-832-62	Sequence 62, Appl
42	21	70.0	6	22	US-09-808-832-65	Sequence 65, Appl
43	21	70.0	6	22	US-09-808-832-71	Sequence 71, Appl
44	21	70.0	6	22	US-09-808-832-73	Sequence 73, Appl
45	21	70.0	6	22	US-09-808-832-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-09-464-908-1
; Sequence 1, Application US/09464908
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Inc.
; TITLE OF INVENTION: Selective Inhibitors Of MMP-12
; FILE REFERENCE: HMR2026A
; CURRENT APPLICATION NUMBER: US/09/464,908
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/155,223
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-464-908-1

Query Match 100.0%; Score 30; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglar 6

Db 1 PLGLAR 6

RESULT 2

US-09-496-231A-31
; Sequence 31, Application US/09496231A

GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Elbert, Donald
; APPLICANT: Lutolf, Matthias
; APPLICANT: Pratt, Allison
; APPLICANT: Schoenmakers, Ronald
; APPLICANT: Tirelli, Nicola
; APPLICANT: Vernon, Brent
; TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC
; TITLE OF INVENTION: ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS
; FILE REFERENCE: 50154/002002
; CURRENT APPLICATION NUMBER: US/09/496,231A
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-496-231A-31

Query Match 83.3%; Score 25; DB 18; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | | |
Db 1 PLGLA 5

RESULT 3

US-09-808-832-75
; Sequence 75, Application US/09808832
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their ther
; TITLE OF INVENTION: use
; FILE REFERENCE: PH-7134
; CURRENT APPLICATION NUMBER: US/09/808,832
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,387
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: acetyl-glycine
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(6)
; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A pep
; OTHER INFORMATION: tide synthesizer using readily available materials well known to
; OTHER INFORMATION: ordinarily skilled artisans
US-09-808-832-75

Query Match 83.3%; Score 25; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | | |
Db 2 PLGLA 6

RESULT 4

US-09-496-231A-29
; Sequence 29, Application US/09496231A
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Elbert, Donald
; APPLICANT: Lutolf, Matthias
; APPLICANT: Pratt, Allison
; APPLICANT: Schoenmakers, Ronald
; APPLICANT: Tirelli, Nicola
; APPLICANT: Vernon, Brent
; TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC
; TITLE OF INVENTION: ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS
; FILE REFERENCE: 50154/002002
; CURRENT APPLICATION NUMBER: US/09/496,231A
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/118,093
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-496-231A-29

Query Match 76.7%; Score 23; DB 18; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgla 5
| | | | |
Db 1 PLGLA 5

RESULT 5

US-09-101-167-23
; Sequence 23, Application US/09101167A
; GENERAL INFORMATION:
; APPLICANT: TE KOPPELE, Johannes M
; APPLICANT: BEERMAN, Bob
; TITLE OF INVENTION: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING
; TITLE OF INVENTION: FLUORESCENCE-QUENCHED SUBSTRATES
; FILE REFERENCE: TE KOPPELE et al. 09/101,167
; CURRENT APPLICATION NUMBER: US/09/101,167A
; CURRENT FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: EP 96200017.0
; EARLIER FILING DATE: 1996-01-04
; EARLIER APPLICATION NUMBER: PCT/NL97/00002
; EARLIER FILING DATE: 1997-01-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:UNKNOWN
US-09-101-167-23

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 6

US-09-168-010-15
; Sequence 15, Application US/09168010

GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
US-09-168-010-15

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 7
US-09-168-010-20
Sequence 20, Application US/09168010
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-168-010-20

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 8
US-09-168-010-21
Sequence 21, Application US/09168010
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal succinyl group
US-09-168-010-21

Query Match 70.0%; Score 21; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 9
US-09-343-650-15
Sequence 15, Application US/09343650
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Meers, Paul
APPLICANT: Pak, Charles
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
TITLE OF INVENTION: Liposomal Drug Delivery
FILE REFERENCE: TLC 215c
CURRENT APPLICATION NUMBER: US/09/343,650
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 08/950,618
EARLIER FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
US-09-343-650-15

Query Match 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 10

US-09-343-650-20
; Sequence 20, Application US/09343650
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Meers, Paul
; APPLICANT: Pak, Charles
; APPLICANT: Ali, Shaikat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
; FILE REFERENCE: TLC 215c
; CURRENT APPLICATION NUMBER: US/09/343,650
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 08/950,618
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-343-650-20

Query Match 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 11

US-09-343-650-21
; Sequence 21, Application US/09343650
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Meers, Paul
; APPLICANT: Pak, Charles
; APPLICANT: Ali, Shaikat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
; FILE REFERENCE: TLC 215c
; CURRENT APPLICATION NUMBER: US/09/343,650
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 08/950,618
; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides

; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
US-09-343-650-21

Query Match 70.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 12

US-09-704-251-13
; Sequence 13, Application US/09704251
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lilly
; APPLICANT: Cook, Charles M.
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; FILE REFERENCE: PPI-106
; CURRENT APPLICATION NUMBER: US/09/704,251
; CURRENT FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-09-704-251-13

Query Match 70.0%; Score 21; DB 21; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 13

US-09-808-832-203
; Sequence 203, Application US/09808832
; GENERAL INFORMATION:
; APPLICANT: DuPont Pharmaceuticals Company
; TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their t
; FILE REFERENCE: PH-7134
; CURRENT APPLICATION NUMBER: US/09/808,832
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/189,387
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 203
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(4)
; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A
; OTHER INFORMATION: tide synthesizer using readily available materials well known
; OTHER INFORMATION: ordinarily skilled artisans

US-09-808-832-203

Query Match 70.0%; Score 21; DB 22; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 14

US-09-972-772-13

; Sequence 13, Application US/09972772

; GENERAL INFORMATION:

; APPLICANT: Olson, Gary L.

; APPLICANT: Self, Christopher

; APPLICANT: Lee, Lily

; APPLICANT: Cook, Charles M.

; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE

; FILE REFERENCE: PPI-106CP

; CURRENT APPLICATION NUMBER: US/09/972,772

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: US 09/704,251

; PRIOR FILING DATE: 2000-11-01

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Motifs

US-09-972-772-13

Query Match

70.0%; Score 21; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 15

US-09-808-832-8

; Sequence 8, Application US/09808832

; GENERAL INFORMATION:

; APPLICANT: DuPont Pharmaceuticals Company

; TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their ther

; TITLE OF INVENTION: use

; FILE REFERENCE: PH-7134

; CURRENT APPLICATION NUMBER: US/09/808,832

; CURRENT FILING DATE: 2001-03-15

; PRIOR APPLICATION NUMBER: 60/189,387

; PRIOR FILING DATE: 2000-03-15

; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(5)

; OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A pep

; OTHER INFORMATION: tide synthesizer using readily available materials well known to

; OTHER INFORMATION: ordinarily skilled artisans

US-09-808-832-8

Query Match 70.0%; Score 21; DB 22; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

Search completed: February 28, 2002, 16:53:15
Job time: 180 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:50:35 ; Search time 14.07 Seconds
(without alignments)
24.143 Million cell updates/sec

Title: 09-876091

Perfect score: 30

Sequence: 1 plglar 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 258822 seqs, 56616433 residues

Total number of hits satisfying chosen parameters: 12908

Minimum DB seq length: 0

Maximum DB seq length: 6

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*

- 1: /cgn2_5/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_5/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_5/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_5/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_5/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_5/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_5/ptodata/2/paa/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	70.0	4	6 US-10-001-945-13	Sequence 13, Appl
2	21	70.0	5	5 US-09-560-390-32	Sequence 32, Appl
3	21	70.0	6	5 US-09-560-390-22	Sequence 22, Appl
4	21	70.0	6	5 US-09-560-390-25	Sequence 25, Appl
5	21	70.0	6	5 US-09-998-831-24	Sequence 24, Appl
6	17	56.7	4	5 US-09-451-206-17	Sequence 17, Appl
7	17	56.7	4	5 US-09-914-541-22	Sequence 22, Appl
8	17	56.7	4	6 US-10-001-945-1	Sequence 1, Appl
9	17	56.7	4	6 US-10-001-945-14	Sequence 14, Appl
10	17	56.7	4	6 US-10-001-945-27	Sequence 27, Appl
11	17	56.7	5	1 PCT-US01-27692A-71	Sequence 71, Appl
12	17	56.7	5	1 PCT-US01-27702A-256	Sequence 256, App
13	17	56.7	5	5 US-09-560-390-2	Sequence 2, Appl
14	17	56.7	5	5 US-09-560-390-18	Sequence 18, Appl
15	17	56.7	5	5 US-09-560-390-21	Sequence 21, Appl
16	17	56.7	5	5 US-09-560-390-24	Sequence 24, Appl
17	17	56.7	5	5 US-09-104-337A-321	Sequence 321, App
18	17	56.7	6	5 US-09-560-390-5	Sequence 5, Appl
19	17	56.7	6	5 US-09-155-613A-91	Sequence 91, Appl
20	16	53.3	5	1 PCT-US01-28044A-364	Sequence 364, Appl
21	15	50.0	5	5 US-09-560-390-19	Sequence 19, Appl
22	15	50.0	6	1 PCT-US01-27702A-268	Sequence 268, App
23	15	50.0	6	5 US-09-604-145-5	Sequence 5, Appl
24	15	50.0	6	6 US-10-001-945-19	Sequence 19, Appl
25	15	50.0	6	6 US-10-001-945-19	Sequence 19, Appl
26	14	46.7	3	1 PCT-US01-28044A-363	Sequence 363, Appl

27	14	46.7	4	1 PCT-US01-47556-62	Sequence 62, Appl
28	14	46.7	4	5 US-09-520-394B-8933	Sequence 8933, Ap
29	14	46.7	4	5 US-09-879-442A-27	Sequence 27, Appl
30	14	46.7	4	5 US-09-879-442A-28	Sequence 28, Appl
31	14	46.7	4	5 US-09-879-442A-29	Sequence 29, Appl
32	14	46.7	4	5 US-09-637-780B-1203	Sequence 1203, App
33	14	46.7	4	5 US-09-708-427-587	Sequence 587, App
34	14	46.7	4	5 US-09-520-111B-9145	Sequence 9145, Ap
35	14	46.7	4	5 US-09-856-819A-15	Sequence 15, Appl
36	14	46.7	4	5 US-09-914-541-21	Sequence 21, Appl
37	14	46.7	4	5 US-09-594-595B-2895	Sequence 2895, Ap
38	14	46.7	4	5 US-09-617-525D-616	Sequence 616, App
39	14	46.7	4	5 US-09-570-582B-775	Sequence 775, App
40	14	46.7	4	5 US-09-607-081B-616	Sequence 616, App
41	14	46.7	4	5 US-09-508-960B-616	Sequence 616, App
42	14	46.7	4	5 US-09-645-441C-587	Sequence 587, App
43	14	46.7	4	5 US-09-857-454-587	Sequence 587, App
44	14	46.7	4	6 US-10-007-761-62	Sequence 62, Appl
45	14	46.7	5	5 US-09-998-909-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-001-945-13
; Sequence 13, Application US/10001945
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; APPLICANT: Birktoft, Jens
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP2
; CURRENT APPLICATION NUMBER: US/10/001,945
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 09/972,772
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-13

Query Match 70.0%; Score 21; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 2
US-09-560-390-32
; Sequence 32, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-32

Query Match 70.0%; Score 21; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 3
US-09-560-390-22
; Sequence 22, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-22

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 4
US-09-560-390-25
; Sequence 25, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-25

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 plgl 4
| | | |

Db 1 PLGL 4

RESULT 5
US-09-998-831-24
; Sequence 24, Application US/09998831
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
; TITLE OF INVENTION: INHIBITING VEGF
; FILE REFERENCE: 4001.002584
; CURRENT APPLICATION NUMBER: US/09/998,831
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/561,108
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-998-831-24

Query Match 70.0%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
| | | |
Db 1 PLGL 4

RESULT 6
US-09-451-206-17
; Sequence 17, Application US/09451206
; GENERAL INFORMATION:
; APPLICANT: STEDRONSKY, Erwin R.
; TITLE OF INVENTION: Tissue Adhesive Using Synthetic
; CROSSLINKING
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: Four Embarcadero Center, Suite 200
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/451,206
; FILING DATE: 29-Nov-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,246
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A61127-1/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-451-206-17

Query Match 56.7%; Score 17; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
Db 1 PLG 3

RESULT 7
US-09-914-541-22
Sequence 22, Application US/09914541
GENERAL INFORMATION:
APPLICANT: THE UNIVERSITY OF TENNESSEE RESEARCH CORPORATION
APPLICANT: BECKER, JEFFREY M.
APPLICANT: HAUSER, MELINDA
APPLICANT: DONHARDT, AMY
APPLICANT: BARNES, DAVID
TITLE OF INVENTION: EUKARYOTIC PEPTIDE UPTAKE SYSTEM FOR TRANSPORTING
TITLE OF INVENTION: ENKEPHALINS
FILE REFERENCE: 1046-PCT-00
CURRENT APPLICATION NUMBER: US/09/914,541
CURRENT FILING DATE: 2001-08-29
PRIOR APPLICATION NUMBER: PCT/US00/05158
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/122,312
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 22
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Tyr-Mif-1
US-09-914-541-22

Query Match 56.7%; Score 17; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
Db 2 PLG 4

RESULT 8
US-10-001-945-1
Sequence 1, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
FILE REFERENCE: PPI-106CP2
CURRENT APPLICATION NUMBER: US/10/001,945
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 09/972,772
PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: US 09/704,251
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: Xaa at position 4 may be any amino acid
OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-1

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
Db 1 PLG 3

RESULT 9
US-10-001-945-14
Sequence 14, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
FILE REFERENCE: PPI-106CP2
CURRENT APPLICATION NUMBER: US/10/001,945
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 09/972,772
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 09/704,251
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-14

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
Db 1 PLG 3

RESULT 10
US-10-001-945-27
Sequence 27, Application US/10001945
GENERAL INFORMATION:
APPLICANT: Olson, Gary L.
APPLICANT: Self, Christopher
APPLICANT: Lee, Lily
APPLICANT: Cook, Charles M.
APPLICANT: Birtkopf, Jens
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE

; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPI-106CP2
; CURRENT APPLICATION NUMBER: US/10/001.945
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 09/972.772
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704.251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
US-10-001-945-27

Query Match 56.7%; Score 17; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4

RESULT 11
PCT-US01-27692A-71
; Sequence 71, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(5)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-71

Query Match 56.7%; Score 17; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 3 PLG 5

RESULT 12
PCT-US01-27702A-256
; Sequence 256, Application PC/TUS0127702A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27702A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 256
; LENGTH: 5
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(5)
; OTHER INFORMATION: synthetic construct
PCT-US01-27702A-256

Query Match 56.7%; Score 17; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 3 PLG 5

RESULT 13
US-09-560-390-2
; Sequence 2, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-2

Query Match 56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4

RESULT 14
US-09-560-390-18
; Sequence 18, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560.390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-18

Query Match 56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plg 3
|||
Db 2 PLG 4


```

RESULT 15
US-09-560-390-21
; Sequence 21, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-21

```

```

Query Match      56.7%; Score 17; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plg 3
   111
Db 1 PLG 3

```

Search completed: February 28, 2002, 16:55:13
Job time: 278 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2002, 16:49:25 ; Search time 12.46 seconds
(without alignments)
10.836 Million cell updates/sec

Title: 09-876091
Perfect score: 30
Sequence: 1 pliglar 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 27062

Minimum DB seq length: 0
Maximum DB seq length: 6

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	76.7	6	2	US-08-747-137-84
2	21	70.0	4	3	US-08-950-618-15
3	21	70.0	4	3	US-08-950-618-20
4	21	70.0	4	3	US-08-950-618-21
5	21	70.0	4	3	US-09-101-167-23
6	21	70.0	4	4	US-09-168-010-15
7	21	70.0	4	4	US-09-168-010-20
8	21	70.0	4	4	US-09-168-010-21
9	21	70.0	6	1	US-08-303-270-8
10	21	70.0	6	4	US-09-208-684-12
11	21	70.0	6	4	US-08-281-313-8
12	19	63.3	6	2	US-08-520-455A-7
13	19	63.3	6	3	US-09-008-308-50
14	18	60.0	5	4	US-08-793-701-9
15	18	60.0	6	1	US-08-014-979-97
16	18	60.0	6	2	US-08-213-897A-17
17	18	60.0	6	2	US-08-188-583-47
18	18	60.0	6	3	US-08-997-918-54
19	18	60.0	6	3	US-09-008-308-60
20	17	56.7	4	1	US-08-219-156-5
21	17	56.7	4	1	US-08-238-089-5
22	17	56.7	4	1	US-08-238-089-6
23	17	56.7	4	1	US-08-366-783-8
24	17	56.7	4	1	US-08-432-651A-5
25	17	56.7	4	1	US-08-432-651A-6
26	17	56.7	4	2	US-08-707-237A-97
27	17	56.7	4	2	US-08-846-021A-11

28	17	56.7	4	3	US-08-642-246-17	Sequence 17, Appl
29	17	56.7	4	3	US-08-962-962C-5	Sequence 5, Appli
30	17	56.7	4	3	US-08-962-962C-6	Sequence 6, Appli
31	17	56.7	4	5	PCT-US95-05560-5	Sequence 5, Appli
32	17	56.7	4	5	PCT-US95-05560-6	Sequence 6, Appli
33	17	56.7	4	5	PCT-US96-06229-17	Sequence 17, Appl
34	17	56.7	5	1	US-08-221-582A-4	Sequence 4, Appli
35	17	56.7	5	1	US-08-219-156-2	Sequence 2, Appli
36	17	56.7	5	1	US-08-219-156-4	Sequence 4, Appli
37	17	56.7	5	1	US-08-219-156-6	Sequence 6, Appli
38	17	56.7	5	1	US-08-219-156-7	Sequence 7, Appli
39	17	56.7	5	1	US-08-219-156-8	Sequence 8, Appli
40	17	56.7	5	1	US-08-238-089-31	Sequence 31, Appl
41	17	56.7	5	1	US-08-238-089-32	Sequence 32, Appl
42	17	56.7	5	1	US-08-213-897A-4	Sequence 4, Appli
43	17	56.7	5	1	US-08-213-897A-15	Sequence 15, Appl
44	17	56.7	5	1	US-08-432-651A-31	Sequence 31, Appl
45	17	56.7	5	1	US-08-432-651A-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-747-137-84
; Sequence 84, Application US/08747137
; Patent No. 5945033
; GENERAL INFORMATION:
; APPLICANT: YEN, Richard C.K.
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,137
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,546
; FILING DATE: 14-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/069,831
; FILING DATE: 01-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,560
; FILING DATE: 13-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/641,720
; FILING DATE: 15-JAN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 016197-000840US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

US-08-747-137-84

FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010A
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-168-010-20

Query Match 70.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 6
US-09-168-010-15
Sequence 15, Application US/09168010A
Patent No. 6143716
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010A
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
US-09-168-010-15

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 7
US-09-168-010-20
Sequence 20, Application US/09168010A
Patent No. 6143716
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same

FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010A
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal methoxy succinyl group
US-09-168-010-20

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 8
US-09-168-010-21
Sequence 21, Application US/09168010A
Patent No. 6143716
GENERAL INFORMATION:
APPLICANT: The Liposome Company Inc.
APPLICANT: Pak, Charles
APPLICANT: Meers, Paul
APPLICANT: Ali, Shaukat
APPLICANT: Janoff, Andrew S.
APPLICANT: Franklin, J. Craig
APPLICANT: Erukulla, Ravi K.
APPLICANT: Cabral-Lilly, Donna
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
TITLE OF INVENTION: Delivery Using Same
FILE REFERENCE: TLC 215B
CURRENT APPLICATION NUMBER: US/09/168,010A
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US 60/027,544
EARLIER FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 4
TYPE: PRT
ORGANISM: Peptides
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)...(1)
OTHER INFORMATION: N-terminal succinyl group
US-09-168-010-21

Query Match 70.0%; Score 21; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PLGL 4

RESULT 9
US-08-303-270-8
Sequence 8, Application US/08303270
Patent No. 5646027

;
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Gelatinase Catalytic Domain Protein
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,270
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 5120-FJT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Thiolester-bond
; LOCATION: 3..4
; US-08-303-270-8

Query Match 70.0%; Score 21; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 10
US-09-208-684-12
; Sequence 12, Application US/09208684
; Patent No. 6224903
; GENERAL INFORMATION:
; APPLICANT: Francis J. Martin
; APPLICANT: Samuel Zalipsky
; TITLE OF INVENTION: Polymer-Lipid Conjugate for Fusion of
; FILE REFERENCE: 5325-0148.32
; CURRENT APPLICATION NUMBER: US/09/208,684
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 08/949,046
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: 60/028,269
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT

;
; ORGANISM: Homo Sapiens
; US-09-208-684-12
;
; Query Match 70.0%; Score 21; DB 4; Length 6;
; Best Local Similarity 100.0%; Pred. No. 1.6e+05;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 plgl 4
; Db 1 PLGL 4
;
; RESULT 11
; US-08-281-313-8
; Sequence 8, Application US/08281313
; Patent No. 6284513
; GENERAL INFORMATION:
; APPLICANT: Ye, Qi-Zhuang
; APPLICANT: Johnson, Linda L.
; APPLICANT: Hupe, Donald J.
; APPLICANT: Baragi, Vijaykumar
; TITLE OF INVENTION: Process for the Production of
; TITLE OF INVENTION: Stromelysin Catalytic Domain Protein
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Warner-Lambert Company
; STREET: 2800 Plymouth Rd.
; CITY: Ann Arbor
; STATE: MI
; COUNTRY: US
; ZIP: 48105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,313
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012,705
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Tinney, Francis J.
; REGISTRATION NUMBER: 33,069
; REFERENCE/DOCKET NUMBER: 4415-01-FJT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 313 996-7295
; TELEFAX: 313 996-1553
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Thiolester-bond
; LOCATION: 3..4
; US-08-281-313-8

Query Match 70.0%; Score 21; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
Db 1 PLGL 4

RESULT 12
US-08-520-455A-7
; Sequence 7, Application US/08520455A
; Patent No. 5872207
; GENERAL INFORMATION:
; APPLICANT: Morgan, Barry Arnold
; APPLICANT: Ator, Mark Alan
; APPLICANT: Gainer, James Arthur
; APPLICANT: Gordon, Thomas Douglas
; APPLICANT: Kruse, Lawrence Ivan
; APPLICANT: Sishaan, Teruna Jaya
; TITLE OF INVENTION: N-terminal Marked Peptides Immobilized
; TITLE OF INVENTION: on Glass beads and Method of Preparation and Method of Use The
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sanofi Pharmaceuticals, Inc.
; STREET: 9 Great Valley Parkway, P.O. Box 3026
; CITY: Malvern
; STATE: PA
; COUNTRY: USA
; ZIP: 19355
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: Dell Optiplex GXi
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: Microsoft Word 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,455A
; FILING DATE: August 29, 1995
; CLASSIFICATION: 530
; APPLICATION NUMBER: US/08/520,455A
; FILING DATE: September 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William J. Davis
; REGISTRATION NUMBER: 30,744
; REFERENCE/DOCKET NUMBER: 61887-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 889-8802
; TELEFAX: (610) 889-8799
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-520-455A-7

Query Match 63.3%; Score 19; DB 2; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plgla 5
Db 2 PLALA 6

RESULT 13
US-09-008-308-50
; Sequence 50, Application US/09008308
; Patent No. 6080575
; GENERAL INFORMATION:
; APPLICANT: Heidtmann, Hans H.
; APPLICANT: Mueller, Rolf
; APPLICANT: Sedlacek, Hans-Harald
; TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
; TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,308
FILING DATE: 16-JAN-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197 01 141.1
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-008-308-50

Query Match 63.3%; Score 19; DB 3; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plgla 5
Db 2 PQGLA 6

RESULT 14
US-08-793-701-9
; Sequence 9, Application US/08793701
; Patent No. 6248581
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, Brigitte
; APPLICANT: LIM, Eng Mong
; APPLICANT: PORTNOI, Denis
; APPLICANT: BERTHET, Francois-Xavier
; APPLICANT: TIMM, Juliano
; TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR
; TITLE OF INVENTION: EXPRESSION VECTORS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &
; ADDRESSEE: DUNNER, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,701
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR9501133
;; FILING DATE: 30-AUG-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 94/10585
;; FILING DATE: 02-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDonnell, Leslie A.
;; REGISTRATION NUMBER: 34,872
;; REFERENCE/DOCKET NUMBER: 02356.0075
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4132
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-793-701-9

Query Match 60.0%; Score 18; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. NO. 1.6e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plgl 4
Db 1 PVGL 4

RESULT 15
US-08-014-979-97
; Sequence 97, Application US/08014979
; Patent No. 5510240
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S. et al.
; TITLE OF INVENTION: Random Bio-Oligomer Library, A Method of
; TITLE OF INVENTION: Synthesis Thereof, and a Method of Use Thereof
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,979
; FILING DATE: 19930208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7156-041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-014-979-97

Query Match 60.0%; Score 18; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plgla 5
Db 2 PYGMA 6

Search completed: February 28, 2002, 16:51:19
Job time: 114 sec

